SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Malcolm, Bruce Taremi, Shahriar S. Weber, Patricia

Yao, Nanhua

- (ii) TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus NS3 Protease and NS4A Cofactor Peptide
- (iii) NUMBER OF SEQUENCES: 123
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Schering-Plough Corp.
 - (B) STREET: 2000 Galloping Hill Road
 - (C) CITY: Kenilworth
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07030
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Power Macintosh
 - (C) OPERATING SYSTEM: 8.0./1
 - (D) SOFTWARE: Microsoft Word 6.0.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: McLaughlin, Jaye P.
 - (B) REGISTRATION NUMBER: 41,211
 - (C) REFERENCE/DOCKET NUMBER: JB0800P2
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (90/8)298-5056
 - (B) TELEFAX: (908/298-5388
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOL ϕ GY: linear
 - (ii) MOLECULE TPPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110 .

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser .* 210 215

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu

ID

20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser 210 215

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

35 40 45

Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 175

Pro Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser 210 215

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val

50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser * 210 215

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala

65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg .130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
165 170 175 .

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser 210 215

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser

85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

- Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125
- Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140
- His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160
- Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
 165 170 175
- Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190
- Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205
- Ser Met Glu Thr Thr Met Arg Ser 210 215

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

 1 5 10 15
- Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30
- Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45
- Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val50 55 60
- Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80
- Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95
- Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn

100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
165 170 175

Pro Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205 .

Ser Met Glu Thr Thr Met Arg Ser 210 215

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser

115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

- His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160
- Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
 165 170 175
- Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190
- Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205
- Ser Met Glu Thr Thr Met Arg Ser 210 215

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

 1 1 5 15
- Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30
- Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45
- Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50 55 60
- Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80
- Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95
- Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110
- Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
165 170 175

Pro Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser * 210 215

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140 His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 175

Pro Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser * 210 215

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 185 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 200 Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 235 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 250 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 280 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 390 400 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 440 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr

465 470 475 480 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 560 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 Cys Met Ser Ala Asp Leu Glu Val Val

(2) INFORMATION FOR SEQ ID NO:12:

660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

35 40

Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 55 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 90 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 120 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 170 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 205 Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 215 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 240 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 295 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 320 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 330

Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu

345

340

Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 365

Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 380

Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400

Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415

Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430

Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445

Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460

Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465. 470 475 480

Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
485 490 495

Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575

Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val 660 665

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

 1 5 10 15
- Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30
- Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45
- Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60
- Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80
- Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95
- Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110
- Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125
- Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140
- His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160
- Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 175
- Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190
- Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205
- Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220

Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 265 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 280 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 310 315 Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 345 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 365 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 375 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 410 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala 435 445 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 455 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 495 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 505 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr

525

530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560

- Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His
 565 570 575
- Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590
- Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605
- Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620
- Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640
- Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655
- Cys Met Ser Ala Asp Leu Glu Val Val 660 665

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

 1 5 10 15
- Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30
- Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45
- Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60
- Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65 70 75 80
- Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95
- Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn

100 105 110 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 135 His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 155 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 175 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 185 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 205 Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 250 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 310 Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 360 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu

410

405

Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430

Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445

Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460

Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480

Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 495

Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575

Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val 660 665

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205

Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220

Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 240

Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln
245 250 255

Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270

Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 280 285

Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 300

Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 320

Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 335

Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 350

Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 365

Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 380

Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400

Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415

Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430

Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala 435 440 445

Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460

Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480

Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 495

Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575

Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala

595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val 660 665

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40

Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Sér 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly

165 170 175 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 215 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 230 235 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 250 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 265 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 295 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 330 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 345 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 375 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 395 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 440 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 470 475

Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 495

Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 550 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575

Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val 660 665

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45

Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly 165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
195 200 205

Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220

Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro 225 230 235 240

Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 255

Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 270

Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 275 280 285

Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 . 300

Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 320

Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 335

Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 350

Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 365

Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 380

Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400

Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415

Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val
420 425 430

Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445

Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn-450 455 460

Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480

Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg
485 490 495

Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510

Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525

Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575

Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val

660 665

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 665 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

 1 5 10 15
- Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu. 20 25 30
- Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu $35 \hspace{1cm} 40 \hspace{1cm} 45$
- Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60
- Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80
- Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
- Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110
- Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125
- Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140
- His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160
- Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
 165 170 175
- Pro Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190
- Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
 195 200 205
- Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser 210 215 220
- Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro

225 230 235 240 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln 245 250 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 280 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 315 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 330 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 360 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 380 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala 440 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 470 480 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560

Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575

.Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590

Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 605

Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 620

Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 640

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 650 655

Cys Met Ser Ala Asp Leu Glu Val Val 660 665

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile
20 25 30

Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser 35 40 45

Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly 50 55 60

Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Ser Thr Ala 65 70 75 80

Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val 85 90 95

Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile 100 105 110 Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala 115 120 125

Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp 130 135 140

Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg 145 150 155 160

Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu
165 170 175

Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val . 180 185 190

Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val 195 200 205

Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val 210 215 220

Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val 225 230 235 240

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro 245 250 255

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser 260 265 270

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly 275 280 285

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala 290 295 300

Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys 305 310 310 315 320

Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr 325 330 335

Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu 340 345 350

Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly 355 360 365

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn 370 380

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile 385 390 395 400

Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp 405 410 415

Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr 420 425 430

Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val 435 440 445

Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp 450 455 460

Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser 470 475 480

Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala 485 490 495

Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Gly 500 505 510

Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp 515 520 525

Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu 530 535 540

Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr 545 550 555 560

Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val 565 570 575

Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys 580 585 590

Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val 595 600 605

Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys 610 615 620

Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu 625 630 635 640

Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile 645 650 655

Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val 660 665 670

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile 20 25 30

Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser 35 40 45

Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly . 50 55 60

Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala 65 70 75 80

Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val 85 90 95

Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile 100 105 110

Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala 115 120 125

Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp 130 135 140

Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg 145 150 155 160

Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu 165 170 175

Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val 180 185 190

Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val 195 200 205

Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val 210 215 220

Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val 225 230 235 240

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro 245 250 255

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser 260 265 270

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly 275 280 285

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala

290 295 300

Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys 315 Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr 325 330 Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly 360 365 Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn 375 Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile 390 395 Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Cys Asp 410 Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr 425 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val 440 Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp 450 455 Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser 470 475 Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala 485 490 Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Gly 505 Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp 520 Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu 530 Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val 565 570 Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys 580

Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val 600

Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys 610 615 620

Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu 625 630 635 640

Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile 645 650 655

Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val 660 665 670

- (2) INFORMATION FOR SEQ ID NO:21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ser Gly Ser 1

- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Pro Ala Gly Gly

- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1964 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1964

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 632 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
- Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly 1 5 10 15
- Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly 20 25 30
- Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys 35 40 45
- Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr 50 55 60.
- Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp 65 70 75 80
- Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr 85 90 95
- Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala 100 105 110
- Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu 115 120 125
- Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu 130 135 140
- Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys 145 150 155 160
- Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met 165 170 175
- Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro 180 185 190
- Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly
 195 200 205

Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr 210 215 220

Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly 225 230 230 235

Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly 245 250 255

Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly 260 265 270

Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile 275 280 285

Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile 290 295 300

Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val 305 310 315 320

Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn 325 330 335

Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly 340 345 350

Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe 355 360 365

Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly 370 375 380

Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val 385 390 395 400

Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met 405 410 415

Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys 420 425 430

Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu 435 440 445

Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly 450 455 460

Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly
465 470 475 480

Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr 485 490 495

Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val 500 505 510

Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp 515 520 525

His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp 530 535 540

Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr 545 550 555 560

Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro 565 570 575

Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr 580 585 590

Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn 595 600 605

Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met 610 615 620

Ser Ala Asp Leu Glu Val Val Thr 625 630

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr 1 5 10 15

Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu Ser 20 25 30

Gly Arg Pro Ala Ile Val Pro Asp Arg Glu Leu Leu Tyr Gln Glu Phe 35 40 45

Asp Glu Met Glu Glu Cys 50

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:25:	
Asp 1	Thr Glu Asp Val Val Cys Cys Ser Met Tyr Thr Trp Thr Gly Lys 5 10 15	
(2) INFORM	MATION FOR SEQ ID NO:26:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) I	MOLECULE TYPE: cDNA	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:26:	
	TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTGG TAGTGGTAGT	60
ATCACGGCCT		78
(2) INFORM	ATION FOR SEQ ID NO:27:	7 6
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: cDNA	
	EQUENCE DESCRIPTION: SEQ ID NO:27:	
	TCTCAAGACC GCATAGTAGT TTCCAT	36
	ATION FOR SEQ ID NO:28:	
	EQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

39
39
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

(2)	INFO	RMATION FOR SEQ ID NO:32:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CGGG	GCCT	AC TTGGTTGCAA GAAGACTAGC CTTACAGGC	39
(2)	INFO	RMATION FOR SEQ ID NO:33:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:33:	
GCCT	GTAAG	G CTAGTCTTCT TGCAACCAAG TAGGCCCCG	39
(2)	INFOR	MATION FOR SEQ ID NO:34:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
		SEQUENCE DESCRIPTION: SEQ ID NO:34:	
CTCCT	PACTTO	G AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC	40
(2)	INFOR	MATION FOR SEQ ID NO:35:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
GCAGAGCAGT GGACCACCAG CAGAGCCCTT CAAGTAGGAG	40
(2) INFORMATION FOR SEQ ID NO:36:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:37:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG 3	9
(2) INFORMATION FOR SEQ ID NO:38:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:39:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:40:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:41:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:42:	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 78 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTGGT	60
ATCACGGCCT ACTCCCAA	78
(2) INFORMATION FOR SEQ ID NO:43:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43: CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT (2) INFORMATION FOR SEQ ID NO:44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	36
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:45:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

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(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu 35 40 45

Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu 50 55 60

Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr 65 70 75 80

Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
85 90 95

Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val 100 105 110

Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu 115 120 125

Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His 130 135 140

Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu 145 150 155 160

Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro
165 170 175

Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val 180 185 190

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser 195 200 205 Met Glu Thr Thr Met Arg Ser 215 (2) INFORMATION FOR SEQ ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: Pro Ala Gly (2) INFORMATION FOR SEQ ID NO:48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48: GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTATC 60 ACGGCCTACT CCCAA 75

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

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CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

 1 5 10 15
- Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30
- Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu 35 40 45
- Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu 50 55 60
- Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr 65 70 75 80
- Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys 85 90 95
- Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val 100 105 110
- Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu 115 120 125
- Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His 130 135 140
- Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu 145 150 155 160
- Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro 165 170 175
- Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val 180 185 190
- Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser 195 200 205
- Met Glu Thr Thr Met 210
- (2) INFORMATION FOR SEQ ID NO:51:

39

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC
(2) INFORMATION FOR SEQ ID NO:52:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG
(2) INFORMATION FOR SEQ ID NO:53:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 166 amino acids
(B) TYPE: amino acid (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
Met Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu 1 5 10 15
Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val 20 25 30
Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu 35 40 45
Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln 50 55 60

Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro 65 70 75 80

Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp 85 90 95

Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser 100 105 110

Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu 115 120 125

Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr 130 135 140

Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu 145 150 155 160

Thr Thr Met Arg Ser * 165

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Ser

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTGG TGGTTCTATC

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(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

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- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 30

Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu 35 40 45

Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu 50 55 60

Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr 65 70 75 80

Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
85 90 95

Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val 100 105 110

Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu 115 120 125

Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His 130 135 140

Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu

145 150 155 160 Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro 165 170 Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val 185 Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser 200 Met Glu Thr Thr Met Arg Ser 210 215 (2) INFORMATION FOR SEQ ID NO:58: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58: CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC 39 (2) INFORMATION FOR SEQ ID NO:59: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG 39 (2) INFORMATION FOR SEQ ID NO:60: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 668 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala 1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Lys
20 25 30

Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val
35 40 45

Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn 50 55 60

Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala 65 70 75 80

Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp 85 90 95

Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys
100 105 110

Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val 115 120 125

Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro 130 135 140

Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys 145 150 155 160

Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg 165 170 175

Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr 180 185 190

Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 195 200 205

Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 210 215 220

Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 235 240

Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 245 250 255

Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 270

Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 275 280 285

Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Cys 290 295 300

Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr

305 310 315 320 Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 395 400 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 410 Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly 420 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 440 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 475 Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg 485 490 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 520 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 540 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 550 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 600 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 615 620

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys 645 650 Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg 660 665 (2) INFORMATION FOR SEQ ID NO:61: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61: CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC 39 (2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG 39 (2) INFORMATION FOR SEQ ID NO:63: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 668 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala

1 5 10 15 Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile 20 25 Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val 40 Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala 75 Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys 100 105 Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val 120 Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys 150 155 Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg 170 Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr 180 185 Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 200 Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 215 Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 250 Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 280 285 Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Cys 295 Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr 305 310 315

Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 335

Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 350

Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala 355 360 365

Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 380

Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 405 410 415

Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly
420 425 430

Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 445

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 460

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 465 470 475 480

Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg
485 490 495

Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 510

Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 525

Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 540

Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 560

Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val
565 570 575

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Ser 580 585 590

Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 595 600 605

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 620

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 630 Asp Leu Glu Val Val Thr (2) INFORMATION FOR SEQ ID NO:64: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64: CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC 39 (2) INFORMATION FOR SEQ ID NO:65: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65: GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG 39 (2) INFORMATION FOR SEQ ID NO:66: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 668 amino acids (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala
1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile 20 25 30

Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val 35 40 45

Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn 50 55 60

Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala 65 70 75 80

Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp 85 90 95

Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys 100 105 110

Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val 115 120 125

Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro
130 140

Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys 145 150 155 160

Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg 165 170 175

Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr 180 185 190

Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 195 200 205

Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 210 215 220

Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 235 240

Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 245 250 255

Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 270

Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 275 280 285

Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Cys 290 295 300

Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr 305 310 315 320

Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 335

Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 350

Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala 355 360 365

Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 380

Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 385 390 395 400

Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 405 410 415

Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly 420 425 430

Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 445

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 460

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 465 470 475 480

Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg 485 490 495

Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 510

Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 525

Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 540

Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 560

Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 575

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 580 585 590

Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 595 600 605

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 620

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 635 640

Asp Leu Glu Val Val Thr

(2) INFORMATION FOR SEQ ID NO:67:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
CTCCTACTTG AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC	40
(2) INFORMATION FOR SEQ ID NO:68:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68: GCAGAGCAGT GGACCACCAG CAGAGCCCTT CAAGTAGGAG	40
(2) INFORMATION FOR SEQ ID NO:69:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 668 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala 1 5 10 15	
Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile 20 25 30	
Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val 35 40 45	





- Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn 50 55 60
- Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala 65 70 75 80
- Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp 85 90 95
- Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys
 100 105 110
- Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val 115 120 125
- Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro 130 135 140
- Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys 145 150 155 160
- Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg 165 170 175
- Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr 180 185 190
- Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 195 200 205
- Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 210 215 220
- Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 235 240
- Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 245 250 255
- Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 260 265 270
- Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 275 280 285
- Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Cys 290 295 300
- Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr 305 310 315 320
- Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 330 335
- Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 350
- Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala

355 360 365 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 395 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 410 Thr Ser Gly Asp Val Val Val Ala Thr Asp Ala Leu Met Thr Gly 420 425 430 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 440 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 475 Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg 490 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 510 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 520 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Ser 580 585

Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 . 615 . 620

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 635 640

Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys 645 650 655

Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg 660 665

(2)	INFORMATION	FOR	SEO	ID	NO:70

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTCCGTCATA CCAACTTCCG GAGACGTCGT TGTCG

35

- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: CGACAACGAC GTCTCCGGAA GTTGGTATGA CGGAC

35

- (2) INFORMATION FOR SEQ ID NO:72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala 1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile
20 25 30

Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val
35 40 45

Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn

50 55 60 Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala 70 Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp 85 Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys 105 Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val 120 125 Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys 145 150 155 Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg 170 Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr 185 Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val 195 205 Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly 215 Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val 225 230 Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr 250 Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg 265 Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe 275 Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr 305 310 315 Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 325 335 Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 345 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala 355 360 365

Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 380

Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 385 390 395

Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro
405 410 415

Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly
420 425 430

Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 445

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 460

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 465 470 475 480

Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg
485 490 495

Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 510

Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 525

Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 540

Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 560

Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 575

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 580 585 590

Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 595 600 605

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 615 620

Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 635 640

Asp Leu Glu Val Val Thr *

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOL	ECULE TYPE: cDNA	
(xi) SEQ	UENCE DESCRIPTION: SEQ ID NO:73:	
ACTAAAGTGC CG	GGCTGCCTA CGCAGCCCAA GGG	33
(2) INFORMATI	ION FOR SEQ ID NO:74:	•
(A) (B) (C	UENCE CHARACTERISTICS:) LENGTH: 33 base pairs) TYPE: nucleic acid) STRANDEDNESS: single) TOPOLOGY: linear	
(ii) MOLE	ECULE TYPE: cDNA	
(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:74:	
CCCTTGGGCT GC	GTAGGCAG CCGGCACTTT AGT	33
(2) INFORMATI	ON FOR SEQ ID NO:75:	
(A) (B) (C)	JENCE CHARACTERISTICS: LENGTH: 39 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(ii) MOLE	CCULE TYPE: cDNA	
(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:75:	
CGGGGCCTAC TTG	GGTTGCAA GATCACTAGC CTTACAGGC	39
(2) INFORMATIO	ON FOR SEQ ID NO:76:	
(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 39 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(ii) MOLE	CULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:77:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(with approximately proceed to the control of the c	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:78:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:79:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TÝPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGG

(2) INFORMATION FOR SEQ ID NO:80:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:81:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:82:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:83:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:84:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:85:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	•
CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC	39
(2) INFORMATION FOR SEQ ID NO:86:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

(ii) MOLECULE TYPE: cDNA

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG	39
(2) INFORMATION FOR SEQ ID NO:87:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 96 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
GATATACATA TGGCTTACTC TCTGACTACG GGTTCTGTTG TTATTGTTGG TAGAATTATT	60
TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA	96
(2) INFORMATION FOR SEQ ID NO:88:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
GTGGTGGTGC TCGAGGCTGC CGCGCGCAC CAGCGTAACG ACCTCCAGGT C	51
(2) INFORMATION FOR SEQ ID NO:89:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 96 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
GATATACATA TGGCTTACTC TCTGACTACG GGTTCTGTTG TTATTGTTGG TAGAATTATT	60
TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA	96
(2) INFORMATION FOR SEC ID NO.90.	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGTGGTGCT CGAGGCTGCC GCGCGGCACC AGCGTAACGA CCTCCAGGTC

50

- (2) INFORMATION FOR SEQ ID NO:91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Asp Thr Glu Asp Val Val Ala Cys Ser Met Ser Tyr Thr Trp Tyr Gly

1 10 15

Lys

- (2) INFORMATION FOR SEQ ID NO:92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATG GGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

1 10 15 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu TCT GGT AGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 CTT GGT TGC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 70 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA 432 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC 480 His Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser 150 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT 528 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly 165 170 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC 576 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG 624 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205 TCC ATG GAA ACT ACT ATG CGG TCT TGA 651 Ser Met Glu Thr Thr Met Arg Ser * 210

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 651 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS(B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His	His	CAT His	CAT His	CAT His	CAC His 10	AGC Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	CCG Pro	4	18
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	ATT Ile	TTA Leu	S	96
TCT Ser	GGT Gly	AGT Ser 35	GGT Gly	AGT Ser	ATC Ile	ACG Thr	GCC Ala 40	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 45	CGG Arg	GGC Gly	CTA Leu	14	14
CTT Leu	GGT Gly 50	TGC Cys	AAG Lys	ATC Ile	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	19	2
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	24	.0
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	28	8
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	33	6
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	38	4
													GTC Val			43	2
													AGG Arg			48	0
CTG Leu																52	8

CC# Pro	A CTO	CTC	TGC Cys 180	Pro	TCC Sei	GGG Gly	CAC His	GCT Ala 189	a Val	GGC LGly	ATO	TTC Phe	C CGC e Arg	g Ala	GCC A Ala	576
GTA Val	TGC Cys	ACC Thr 195	Arg	GGG GGG	GTT Val	GCG Ala	AAG Lys 200	. Ala	GTG A Val	GAC L Asp	TTT Phe	GTG ⊇ Val	l Pro	GTA Val	A GAG l Glu	624
		Glu				CGG Arg 21!	g Sei									651
(2)		L) Si	EQUEI (A) I (B) I	NCE (LENGT LYPE:	CHAR CH: (ID 1 ACTER 551 R cleic NESS:	RIST: Dase	ICS: pai: id	rs						. •	•
) MC	(D) 'S DLECU EATUI (A) I	ropoi VLE T RE: VAME/	OGY YPE: KEY:	DNA CDS	near (ge		ic)							
	(xi					IPTI		SEQ	ID N	io:94	:					
ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His 10	AGC Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	ATT Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	ATT Ile	TTA Leu	96
TCT Ser	GGT Gly	AGT Ser 35	GGT Gly	AGT Ser	ATC Ile	ACG Thr	GCC Ala 40	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 45	Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	TGC Cys	ATC Ile	AAG Lys	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336

GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	TCG Ser	GGT Gly 175	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	624
	ATG Met 210				Met			TGA *								651

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His 10	AGC Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	CCG Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	ATT Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	ATT Ile	TTA Leu	96
тст	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	144

Ser	Gly	Ser 35	Gl _y	/ Ser	: Ile	• Thr	Ala 40		Ser	Gln	Glr	Thr 45		ı Gly	/ Leu		
CTT Leu	GGT Gly 50	Cys	Lys	AAG Lys	ACT Thr	AGC Ser 55	Leu	ACA Thr	. GGC : Gly	CGG Arg	GAC Asp	Lys	AAC Asn	CAG Glr	GTC Val	19	2
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	' CAG . Gln	GTG Val	Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	24	C
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	Ser	28	8
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	Thr	AAT Asn	330	5
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384	1
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432	3
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480)
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	TCG Ser	GGT Gly 175	GGT Gly	528	}
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576	i
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	624	:
TCC Ser	ATG Met 210	GAA Glu	ACT Thr	ACT Thr	ATG Met	CGG Arg 215		TGA *								651	

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

								-								
ATG Met 1	GIY	AGO Sei	C AGO	CAT His	His	CAT His	'CAT	CAT His	CAC His	Ser	AGC Sei	C GGC	CTC	GTG u Val	CCG Pro	48
CGC Arg	GGC Gly	AGC Ser	C CAT His	Met	GGT Gly	TCT Ser	GTT Val	GTT Val	. Il∈	' GTT • Val	GGI Gly	AGA Arg	ATI Ile	• I1∈	TTA	. 96
TCT Ser	GGT Gly	AGI Ser 35	Gly	AGT Ser	ATC	ACG Thr	GCC Ala 40	Туг	TCC Ser	CAA Gln	CAG Glr	ACG Thr	Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	Cys	ATC Ile	ATC	ACT Thr	AGC Ser 55	Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp	Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly 175	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG (GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val	CCC Pro	GTA Val	GAG Glu	624

205

432

200

195

TCC ATG GAA ACT ACT ATG CGG TCT 650 Ser Met Glu Thr Thr Met Arg Ser 215 (2) INFORMATION FOR SEQ ID NO:97: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 650 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..650 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97: ATG GGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 5 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 40 CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 55 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 70 75 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA

Leu '	Thr 130	Pro	Cys	Thr	Суз	Gly 135	Ser	Ser	Asp	Leu	Tyr 140		. Val	. Thi	Arg		
CAT (His 1 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG GGG	AGC Ser 160	48	80
CTG (Leu 1	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly 175	Gly	52	28
CCA (CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg	Ala	GCC Ala	57	76
GTA T	rgc Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	Glu	62	24
TCC A							Ser	TG							•	65	50
(2) I																	
	(i)	(<i>I</i> (I	A) LI 3) T C) S	ENGTI YPE: IRAN	H: 6! nuc: DEDN	CTER 51 ba leic ESS: line	ase ; aci sin	pair d	s								
((ii)					cDN											
	(ix)) N2	AME/I	KEY:	CDS	651										
((xi)	SEQ	UENC	E DE	SCRI	PTIC	N: S	SEQ I	ED NO	D:98:	:						
ATG G Met G 1	GC A	AGC A	AGC (Ser 1	CAT His 5	CAT (CAT (CAT His	CAT His	CAC His 10	AGC Ser	AGC (Ser	GGC Gly	CTG Leu	GTG Val 15	CCG Pro	4	8
CGC GG Arg G	GC A	AGC (Ser I	CAT A	ATG (GGT ' Gly	TCT (Ser	GTT (Val	GTT Val 25	ATT (GTT (Val	GGT :	AGA Arg	ATT Ile 30	ATT Ile	TTA Leu	9	6
TCT GG	GT A	AGT (Ser (35	GT A	AGT A	ATC I	ACG (GCC ' Ala 40	TAC Tyr	TCC (Ser	CAA (Gln	CAG /	ACG Thr 45	CGG Arg	GGC Gly	CTA Leu	14	4
CTT G(Leu G	GT 1 ly (50	GC A	ATC A	AAG 1 Lys '	ACT I	AGC (Ser :	CTT /	ACA Thr	GGC (CGG (Arg	GAC A Asp 60	AAG . Lys	AAC Asn	CAG Gln	GTC Val	19:	2

GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gl _Y 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly 175	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
TA /al	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	624
					ATG Met			TGA *								651

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATC Met	- GTZ	C AGO	C AGC Ser	CAT His	His	CAT	CAT His	CAT His	CAC His	Ser	AGC Ser	GGC Gl ₂	CTC Lev	G GTC 1 Va:	G CCG L Pro	48
CGC Arg	GGC GGC	AGC Ser	CAT His 20	Met	GGT Gly	TCT Ser	GTT Val	GTT Val	. Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile	: Ile	TTA E Leu	96
TCI Ser	GGT Gly	AGT Ser 35	GLY	AGT Ser	ATC Ile	ACG Thr	GCC Ala	туг	TCC Ser	CAA Gln	CAG Gln	ACG Thr	Arg	GGC	CTA Leu	144
CTT Leu	GGT Gly 50	Cys	AAG Lys	AAG Lys	ACT Thr	AGC Ser 55	Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	Lys	AAC Asn	CAG Glr	GTC Val	192
GAG Glu 65	GIY	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly 175	GGT Gly	- 528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr 195	CGG (Arg (GGG (GTT (Val	Ala	AAG Lys 200	GCG Ala	GTG (GAC Asp	TTT (GTG Val 205	CCC Pro	GTA Val	GAĢ Glu	624
TCC Ser								TGA *								651

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS(B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His	Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	CCG [.] Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	ATT Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	ATT Ile	TTA Leu	96
TCT Ser	CCT Pro	GCT Ala 35	GGT Gly	GGT Gly	ATC Ile	ACG Thr	GCC Ala 40	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 45	CGG Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	TGC Cys	ATC Ile	ATC Ile	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480

CT(Le	G CT(C TCC	C CCC	AGG Arg 165	r Pro	GTC Val	TCC	TAC Ty	TTC Lei 170	ı Ly:	G GG(S Gl _l	TCT y Se:	TCC r Se	G GGT r Gly 17	GGT Gly	528
CC? Pro	A CTO	G CTC	TGC Cys 180	Pro	TCG Ser	GGG Gly	CAC	GCT Ala 185	a Val	G GGC	C ATO	TTC Phe	C CGG Arg	g Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr	Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	Ala	GTC a Val	G GAC	TTI Phe	GTG Val	Pro	GTA Val	GAG Glu	624
		Glu	ACT Thr				Sea									. 651
(2)	INF	ORMA	TION	FOR	SEQ	ID N	10:10	01:							. •	
	(:		EQUEN (A) L (B) T (C) S (D) T	ENGT TYPE : STRAN	H: 6 nuc IDEDN	51 b leic ESS:	ase aci sir	pain id	rs							
	(ii	.) MC	LECU	LE I	YPE:	CDN	A									
	(i)	(EATUR (A) N (B) L	IAME/												
			QUEN													
ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His 10	AGC Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	CCG Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	ATT Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	ATT Ile	TTA Leu	96
TCT Ser	CCT Pro	GCT Ala 35	GGT Gly	GGT Gly	ATC Ile	ACG Thr	GCC Ala 40	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 45	CGG Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	TGC Cys	AAG Lys	ATC Ile	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly	TCA Ser	288

				85					90					95	i	
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	TCG Ser	GGT Gly 175	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	624
			ACT Thr					TGA *								651
(2)	INFO	RMAT	ION	FOR	SEQ	ID I	NO:1	02:								
	(i)	(I (C	QUENCA) LE B) TY C) ST D) TO	ENGTI (PE : [RANI	H: 19 nucl	998 l Leic ESS:	oase acio sino	pai:	rs							
	(ii)	MOI	LECUI	E T	PE:	cDNA	A									
	(ix)	(]	ATURI A) NA 3) LO	ME/I			995									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 15

48

CGC Arg	GGC Gly	C AGO	CAT His	Met	GGT Gly	TCT Ser	GTT Val	GTT Val	. Ile	GTT Val	GGT Gly	' AGA ' Arg	ATT Ile	: Ile	' TTA e Leu	96
TCI Ser	GGT Gly	AGT Ser 35	Gly	AGT Ser	ATC	ACG Thr	GCC Ala 40	Туг	TCC Ser	CAA Gln	CAG Glr	ACG Thr	Arg	GGC GGC	CTA Leu	144
CTT Leu	GGT Gly 50	Cys	ATC Ile	ATC Ile	ACT Thr	AGC Ser 55	Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp	Lys	AAC Asn	CAG Glr	GTC Val	192
GAG Glu 65	Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	. 240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	TCG Ser	GGT Gly 175	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	624
TCC Ser	ATG Met 210	GAA Glu	ACT Thr	ACT Thr	ATG Met	CGG Arg 215	TCT Ser	CCG Pro	GTC Val	TTC Phe	ACG Thr 220	GAC Asp	AAC Asn	TCA Ser	TCC Ser	672
									GTG Val							720
ACT Thr	GGC Gly	AGC Ser	GGC Gly	AAG Lys	AGT Ser	ACT Thr	AAA Lys	GTG Val	CCG Pro	GCT Ala	GCA Ala	TAT Tyr	GCA Ala	GCC Ala	CAA Gln	768

245 250 255 GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG 816 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly 260 265 TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA 864 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg 280 ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC 912 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC 960 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG 1008 Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGT 1056 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC 1104 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 360 365 CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC 1152 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 375 TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC 1200 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 ATT TTC TGT CAT TCC AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG 1248 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG 1296 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT 1344 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala 435 440 CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC 1392 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 455 ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC 1440 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 470 475

ATT Ile	GAG Glu	ACG Thr	ACG Thr	ACC Thr 485	Val	CCT	CAA Gln	GAC Asp	GCA Ala 490	Val	TCG Ser	CGC Arg	TCG Ser	CAG Gln 495	Arg	1488
CGG Arg	GGT Gly	AGG Arg	ACT Thr 500	GGC Gly	AGG Arg	GGT Gly	AGG Arg	AGA Arg 505	Gly	ATC Ile	TAC Tyr	AGG Arg	TTT Phe 510	Val	ACT Thr	1536
CCG Pro	GGA Gly	GAA Glu 515	CGG Arg	CCC Pro	TCG Ser	GGC Gly	ATG Met 520	Phe	GAT Asp	TCC Ser	TCG Ser	GTC Val 525	Leu	TGT Cys	GAG Glu	1584
TGC Cys	ТАТ Туг 530	GAC Asp	GCG Ala	GGC Gly	TGT Cys	GCT Ala 535	Trp	TAC Tyr	GAG Glu	CTC Leu	ACC Thr 540	CCC Pro	GCC Ala	GAG Glu	ACC Thr	. 1632
TCG Ser 545	GTT Val	AGG Arg	TTG Leu	CGG Arg	GCC Ala 550	TAC Tyr	CTG Leu	AAC Asn	ACA Thr	CCA Pro 555	GGG Gly	TTG Leu	CCC Pro	GTT Val	TGC Cys 560	1680
CAG Gln	GAC Asp	CAC His	CTG Leu	GAG Glu 565	TTC Phe	TGG Trp	GAG Glu	AGT Ser	GTC Val 570	TTC Phe	ACA Thr	GGC Gly	CTC Leu	ACC Thr 575	CAT His	1728
ATA Ile	GAT Asp	GCA Ala	CAC His 580	TTC Phe	TTG Leu	TCC Ser	CAG Gln	ACC Thr 585	AAG Lys	CAG Gln	GCA Ala	GGA Gly	GAC Asp 590	AAC Asn	TTC Phe	1776
CCC Pro	TAC Tyr	CTG Leu 595	GTA Val	GCA Ala	TAC Tyr	CAA Gln	GCC Ala 600	ACG Thr	GTG Val	TGC Cys	GCC Ala	AGG Arg 605	GCT Ala	CAG Gln	GCC Ala	1824
CCA Pro	CCT Pro 610	CCA Pro	TCA Ser	TGG Trp	GAT Asp	CAA Gln 615	ATG Met	TGG Trp	AAG Lys	TGT Cys	CTC Leu 620	ATA Ile	CGG Arg	CTG Leu	AAA Lys	1872
CCT Pro 625	ACG Thr	CTG Leu	CAC His	GGG Gly	CCA Pro 630	ACA Thr	CCC Pro	TTG Leu	CTG Leu	TAC Tyr 635	AGG Arg	CTG Leu	GGA Gly	GCC Ala	GTC Val 640	1920
CAA Gln	AAT Asn	GAG Glu	GTC Val	ACC Thr 645	CTC Leu	ACC Thr	CAC His	CCC Pro	ATA Ile 650	ACC Thr	AAA Lys	TAC Tyr	ATC Ile	ATG Met 655	GCA Ala	1968
		TCG Ser							ACT							1998

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1997

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His 10	Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	CCG Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	ATT Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	Ile	TTA· Leu	96
TCT Ser	GGT Gly	AGT Ser 35	GGT Gly	AGT Ser	ATC Ile	ACG Thr	GCC Ala 40	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 45	CGG Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	TGC Cys	AAG Lys	ATC Ile	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	AĊT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
												TCT Ser				528

CC/ Pro	A CTO	G CTO	TG0 1 Cys 180	s Pro	TCC Sei	G GGG	G CAC	GCT Ala 185	a Val	GGC Gl	ATO	C TTC e Phe	CGG Arg	g Ala	GCC A Ala	576
GT <i>I</i> Val	A TGC Cys	2 ACC 5 Thr 195	r Arç	g Gly	GTT Val	GCG L Ala	AAC Lys 200	: Ala	GTO Val	GAC Asp	TTI Phe	GTG Val 205	. Pro	GTA Val	GAG L Glu	624
TCC Ser	ATC Met 210	: Glu	A ACT	Thr	ATG Met	CGG Arg 215	, Ser	CCG Pro	GTC Val	TTC Phe	ACC Thi	Asp	AAC Asn	TCA Ser	TCC Ser	672
CCC Pro 225	Pro	GCC Ala	GTA Val	CCG Pro	CAG Gln 230	Ser	TTT Phe	CAA Gln	GTG Val	GCC Ala 235	His	CTA Leu	CAC His	GCT Ala	CCC Pro 240	720
ACT Thr	GGC	AGC Ser	GGC Gly	AAG Lys 245	Ser	ACT Thr	AAA Lys	GTG Val	CCG Pro 250	Ala	GCA Ala	TAT Tyr	GCA Ala	GCC Ala 255	Gln	768
GGG Gly	TAC Tyr	AAG Lys	GTG Val 260	Leu	GTC Val	CTC Leu	AAT Asn	CCG Pro 265	TCC Ser	GTT Val	GCC Ala	GCT Ala	ACC Thr 270	Leu	GGG Gly	816
TTT Phe	GGG Gly	GCG Ala 275	Tyr	ATG Met	TCT Ser	AAG Lys	GCA Ala 280	CAC His	GGT Gly	ATT Ile	GAC Asp	CCC Pro 285	AAC Asn	ATC Ile	AGA Arg	864
ACT Thr	GGG Gly 290	GTA Val	AGG Arg	ACC Thr	ATT Ile	ACC Thr 295	ACA Thr	GGC Gly	GCC Ala	CCC Pro	GTC Val 300	ACA Thr	TAC Tyr	TCT Ser	ACC Thr	912
TAT Tyr 305	GGC Gly	AAG Lys	TTT Phe	CTT Leu	GCC Ala 310	GAT Asp	GGT Gly	GGT Gly	TGC Cys	TCT Ser 315	GGG Gly	GGC Gly	GCT Ala	TAT Tyr	GAC Asp 320	960
ATC Ile	ATA Ile	ATA Ile	TGT Cys	GAT Asp 325	GAG Glu	TGC Cys	CAT His	TCA Ser	ACT Thr 330	Asp	TCG Ser	ACT Thr	ACA Thr	ATC Ile 335	Leu	1008
GGC Gly	ATC Ile	GGC Gly	ACA Thr 340	GTC Val	CTG Leu	GAC Asp	CAA Gln	GCG Ala 345	GAG Glu	ACG Thr	GCT Ala	GGA Gly	GCG Ala 350	CGG Arg	CTT Leu	1056
GTC Val	GTG Val	CTC Leu 355	GCC Ala	ACC Thr	GCT Ala	ACG Thr	CCT Pro 360	CCG Pro	GGA Gly	TCG Ser	GTC Val	ACC Thr 365	GTG Val	CCA Pro	CAC His	1104
CCA Pro	AAC Asn 370	ATC Ile	GAG Glu	GAG Glu	GTG Val	GCC Ala 375	CTG Leu	TCT Ser	AAT Asn	ACT Thr	GGA Gly 380	GAG Glu	ATC Ile	CCC Pro	TTC Phe	1152
TAT Tyr 385	GGC Gly	AAA Lys	GCC Ala	ATC Ile	CCC Pro 390	ATT Ile	GAA Glu	GCC . Ala	ATC Ile	AGG Arg 395	GGG Gly	GGA Gly	AGG Arg	CAT His	CTC Leu 400	1200
ATT Ile	TTC Phe	TGT Cys	CAT His	TCC Ser	AAG Lys	AAG Lys	AAG Lys	TGC (Cys	GAC Asp	GAG Glu	CTC Leu	GCC Ala	GCA Ala	AAG Lys	CTG Leu	1248

405 410 415 TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG 1296 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT 1344 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC 1392 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC 1440 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 ATT GAG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG. 1488 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT 1536 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 505 CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG 1584 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 520 TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC 1632 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC 1680 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT 1728 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC 1776 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC 1824 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA 1872 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 615 CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC 1920 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 630 635

CA/ Glr	A AA'	r GAd	G GTO	C ACC 1 Th: 64!	r Le	C ACC	C CAC	C CCC	C ATA O Ile 65	e Thi	C AAA	A TAC	C ATO	C ATO e Me 65	G GCA t Ala 5	1968
				a As		G GAC			1	,						1998
(2)	INF	FORMA	MOITA	I FOR	SEÇ	D	NO:1	04:								
	((A) (B) (C)	LENG TYPE STRA	TH: : nu NDED	ACTE 1998 clei NESS : li	bas c ac : si	e pa id								
	(i:	i) M	OLEC	ULE '	TYPE	: cD	NA									
	(i:			NAME		: CD:		5								
	(xi) SE	EQUEN	ICE I	DESCF	RIPTI	ON:	SEQ	ID N	JO:10	14:					
ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His 10	AGC Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	Ile	TTA Leu	96
TCT Ser	GGT Gly	AGT Ser 35	GGT Gly	AGT Ser	ATC Ile	ACG Thr	GCC Ala 40	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 45	CGG Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	TGC Cys	ATC Ile	AAG Lys	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly	GCG Ala	CGT Arg	TCC Ser	. 384

TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu

GTC Val	GTG Val	CTC Leu 355	Ala	ACC Thr	GCT Ala	ACG Thr	CCT Pro 360	Pro	GGA Gly	TCG Ser	GTC Val	ACC Thr	Val	CCA Pro	CAC His		1104
CCA Pro	AAC Asn 370	Ile	GAG Glu	GAG Glu	GTG Val	GCC Ala 375	CTG Leu	TCT Ser	AAT Asn	ACT Thr	GGA Gly 380	GAG Glu	ATC Ile	CCC Pro	TTC Phe		1152
ТАТ Туг 385	GGC Gly	AAA Lys	GCC Ala	ATC Ile	CCC Pro 390	Ile	GAA Glu	GCC Ala	ATC Ile	AGG Arg 395	GGG Gly	GGA Gly	AGG Arg	CAT His	CTC Leu 400		1200
ATT Ile	TTC Phe	TGT Cys	CAT His	TCC Ser 405	Lys	AAG Lys	AAG Lys	TGC Cys	GAC Asp 410	GAG Glu	CTC Leu	GCC Ala	GCA Ala	AAG Lys 415	Leu	•	1248
TCA Ser	GGC Gly	CTC Leu	GGA Gly 420	ATC Ile	AAC Asn	GCT Ala	GTG Val	GCG Ala 425	ТАТ Туг	TAC Tyr	CGG Arg	GGG Gly	CTC Leu 430	Asp	GTG Val		1296
TCC Ser	GTC Val	ATA Ile 435	CCA Pro	ACT Thr	ATC Ile	GGA Gly	GAC Asp 440	GTC Val	GTT Val	GTC Val	GTG Val	GCA Ala 445	ACA Thr	GAC Asp	GCT Ala		1344
CTG Leu	ATG Met 450	ACG Thr	GGC Gly	TAT Tyr	ACG Thr	GGC Gly 455	GAC Asp	TTT Phe	GAC Asp	TCA Ser	GTG Val 460	ATC Ile	GAC Asp	TGT Cys	AAC Asn		1392
ACA Thr 465	TGT Cys	GTC Val	ACC Thr	CAG Gln	ACA Thr 470	GTC Val	GAC Asp	TTC Phe	AGC Ser	TTG Leu 475	GAT Asp	CCC Pro	ACC Thr	TTC Phe	ACC Thr 480		1440
ATT Ile	GAG Glu	ACG Thr	ACG Thr	ACC Thr 485	GTG Val	CCT Pro	CAA Gln	GAC Asp	GCA Ala 490	GTG Val	TCG Ser	CGC Arg	TCG Ser	CAG Gln 495	CGG Arg		1488
CGG Arg	GGT Gly	AGG Arg	ACT Thr 500	Gly	AGG Arg	GGT Gly	AGG Arg	AGA Arg 505	GGC Gly	ATC Ile	TAC Tyr	AGG Arg	TTT Phe 510	GTG Val	ACT Thr		1536
CCG Pro	GGA Gly	GAA Glu 515	CGG Arg	CCC Pro	TCG Ser	GGC Gly	ATG Met 520	TTC Phe	GAT Asp	TCC Ser	TCG Ser	GTC Val 525	CTG Leu	TGT Cys	GAG Glu		1584
TGC Cys	TAT Tyr 530	GAC Asp	GCG Ala	GGC Gly	TGT Cys	GCT Ala 535	TGG Trp	TAC Tyr	GAG Glu	CTC Leu	ACC Thr 540	CCC Pro	GCC Ala	GAG Glu	ACC Thr		1632
TCG Ser 545	GTT Val	AGG Arg	TTG Leu	CGG Arg	GCC Ala 550	TAC Tyr	CTG Leu	AAC Asn	ACA Thr	CCA Pro 555	GGG Gly	TTG Leu	CCC Pro	GTT Val	TGC Cys 560		1680
												GGC Gly					1728
ATA Ile	GAT Asp	GCA Ala	CAC His	TTC Phe	TTG Leu	TCC Ser	CAG Gln	ACC Thr	AAG Lys	CAG Gln	GCA Ala	GGA Gly	GAC Asp	AAC Asn	TTC Phe		1776

580 585 CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC 1824 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 600 CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA 1872 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 610 615 CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC 1920 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 625 630 635 1968 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 645 TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT 1998 . • Cys Met Ser Ala Asp Leu Glu Val Val 660 (2) INFORMATION FOR SEQ ID NO:105: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1998 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..1995 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105: ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 25 TCT GGT AGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 40 CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC

Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val

55

50

GAG Glu 65	r GTZ	A GAO	G GTT ı Val	CAC Glr	GTC TVal	l Val	TCC Sei	C ACC	C GCA	ACA Thi	Glr	TCC Sei	TTC	CTC	G GCG Ala 80		240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	' Val	G TGT	TGG Trp	G ACC	GTT Val	TAC	CAT	GGT Gly	' GCT ⁄ Ala	GGC Gl _y	TCA Ser		288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro	Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr	Thr	AAT Asn		336
GTG Val	GAC Asp	CAG Gln 115	Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	Ala	CGT Arg	TCC Ser		384
TTG Leu	ACA Thr 130	Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	Leu	GTC Val	ACG Thr	AGA Arg		432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160		480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	TCG Ser	GGT Gly 175	GGT Gly		528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala		576
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	•	624
TCC Ser	ATG Met 210	GAA Glu	ACT Thr	ACT Thr	ATG Met	CGG Arg 215	TCT Ser	CCG Pro	GTC Val	TTC Phe	ACG Thr 220	Asp	AAC Asn	TCA Ser	TCC Ser		672
CCC Pro 225	CCG Pro	GCC Ala	GTA Val	CCG Pro	CAG Gln 230	TCA Ser	TTT Phe	CAA Gln	GTG Val	GCC Ala 235	CAC His	CTA Leu	CAC His	GCT Ala	CCC Pro 240		720
ACT Thr	GGC Gly	AGC Ser	GGC Gly	AAG Lys 245	AGT Ser	ACT Thr	AAA Lys	GTG Val	CCG Pro 250	GCT Ala	GCA Ala	TAT Tyr	GCA Ala	GCC Ala 255	CAA Gln		768
GGG Gly	TAC Tyr	AAG Lys	GTG Val 260	CTC Leu	GTC Val	CTC Leu	AAT Asn	CCG Pro 265	TCC Ser	GTT Val	GCC Ala	GCT Ala	ACC Thr 270	TTA Leu	GGG Gly	;	816
TTT Phe	GGG Gly	GCG Ala 275	TAT Tyr	ATG Met	TCT Ser	AAG Lys	GCA Ala 280	CAC His	GGT Gly	ATT Ile	GAC Asp	CCC Pro 285	AAC . Asn	ATC Ile	AGA Arg	8	864
ACT (GGG Gly	GTA Val	AGG Arg	ACC Thr	ATT Ile	ACC . Thr	ACA Thr	GGC Gly	GCC Ala	CCC Pro	GTC . Val	ACA Thr	TAC ' Tyr	TCT . Ser	ACC Thr	9	912

290 295 300 TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC 960 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 310 315 ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG 1008 Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGT 1056 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC 1104 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC. 1152 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC 1200 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 390 395 ATT TTC TGT CAT TCC AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG 1248 Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 410 TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG 1296 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT 1344 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC 1392 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC 1440 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 ATT GAG ACG ACG GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG 1488 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT 1536 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG 1584 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520

TGC Cys	TAT Tyr 530	Asp	GCG Ala	GGC Gly	TGT Cys	GCT Ala 535	Trp	TAC Tyr	GAG Glu	CTC Leu	ACC Thr 540		GCC Ala	GAG Glu	ACC Thr	16:	32
TCG Ser 545	GTT Val	AGG Arg	TTG Leu	CGG Arg	GCC Ala 550	Tyr	CTG Leu	AAC Asn	ACA Thr	CCA Pro 555	Gly	TTG Leu	CCC Pro	GTT Val	TGC Cys 560	168	80
CAG Gln	GAC Asp	CAC His	CTG Leu	GAG Glu 565	TTC Phe	TGG Trp	GAG Glu	AGT Ser	GTC Val 570	Phe	ACA Thr	GGC Gly	CTC Leu	ACC Thr 575	CAT His	172	28
ATA Ile	GAT Asp	GCA Ala	CAC His 580	TTC Phe	TTG Leu	TCC Ser	CAG Gln	ACC Thr 585	Lys	CAG Gln	GCA Ala	GGA Gly	GAC Asp 590	AAC Asn	TTC Phe	177	76
CCC Pro	TAC Tyr	CTG Leu 595	GTA Val	GCA Ala	TAC Tyr	CAA Gln	GCC Ala 600	ACG Thr	GTG Val	TGC Cys	GCC Ala	AGG Arg 605	GCT Ala	CAG Gln	GCC Ala	182	24
CCA Pro	CCT Pro 610	CCA Pro	TCA Ser	TGG Trp	GAT Asp	CAA Gln 615	ATG Met	TGG Trp	AAG Lys	TGT Cys	CTC Leu 620	ATA Ile	CGG Arg	CTG Leu	AAA Lys	187	'2
CCT Pro 625	ACG Thr	CTG Leu	CAC His	GGG Gly	CCA Pro 630	ACA Thr	CCC Pro	TTG Leu	CTG Leu	TAC Tyr 635	AGG Arg	CTG Leu	GGA Gly	GCC Ala	GTC Val 640	192	0
CAA Gln	AAT Asn	GAG Glu	GTC Val	ACC Thr 645	CTC Leu	ACC Thr	CAC His	CCC Pro	ATA Ile 650	ACC Thr	AAA Lys	TAC Tyr	ATC Ile	ATG Met 655	GCA Ala	196	8
TGC Cys									ACT							199	8

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1998 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro 1 5 10 15

48

CGC Arg	GGC Gly	AGC Ser	CAT His	Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	Ile	GTT Val	GGT Gly	' AGA ' Arg	ATT Ile	Ile	TTA Leu	96
TCI Ser	GGT Gly	AGT Ser 35	Gly	AGT Ser	ATC Ile	ACG Thr	GCC Ala 40	Туг	TCC Ser	CAA Gln	CAG Glr	ACG Thr	Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	Cys	ATC	ATC Ile	ACT Thr	AGC Ser 55	Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly 175	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	624
TCC Ser	ATG Met 210	GAA Glu	ACT Thr	ACT Thr	ATG Met	CGG Arg 215	TCT Ser	CCG Pro	GTC Val	TTC Phe	ACG Thr 220	GAC Asp	AAC Asn	TCA Ser	TCC Ser	672
												CTA Leu				720
ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768

Th:	r Gly	y Sei	r Gly	' Lys 245	s Ser	Th:	. Lys	s Val	l Pro 250		a Ala	а Туг	c Ala	a Ala 25	a Gln 5	
GG(Gl _y	Э ТА(/ Ту:	C AAC	GTG Val 260	Leu	GTC Ual	CTC Lev	AAT Asn	CCG Pro 265	Ser	GTT Val	GCC Ala	GCT Ala	ACC Thi	Lei	A GGG	816
TTT Phe	r GGC e Gly	G GCC 7 Alá 275	ı Tyr	ATC Met	TCT Ser	' AAG	GCA Ala 280	His	GGT Gly	ATT Ile	GAC Asp	CCC Pro 285	Asr	ATC	AGA Arg	864
ACT Thr	GGG Gly 290	r Val	AGG Arg	ACC Thr	ATT	ACC Thr 295	Thr	GGC Gly	GCC Ala	CCC Pro	GTC Val	Thr	TAC	TCT Ser	ACC Thr	912
ТАТ Туг 305	Gly	AAG Lys	TTT Phe	CTT Leu	GCC Ala 310	GAT Asp	GGT Gly	GGT Gly	TGC Cys	TCT Ser 315	GGG Gly	GGC Gly	GCT Ala	ТАТ Туг	GAC Asp 320	960
ATC Ile	ATA Ile	ATA Ile	TGT Cys	GAT Asp 325	GAG Glu	TGC Cys	CAT His	TCA Ser	ACT Thr 330	GAC Asp	TCG Ser	ACT Thr	ACA Thr	ATC Ile	Leu	1008
GGC Gly	ATC Ile	GGC Gly	ACA Thr 340	GTC Val	CTG Leu	GAC Asp	CAA Gln	GCG Ala 345	GAG Glu	ACG Thr	GCT Ala	GGA Gly	GCG Ala 350	Arg	CTT Leu	1056
GTC Val	GTG Val	CTC Leu 355	GCC Ala	ACC Thr	GCT Ala	ACG Thr	CCT Pro 360	CCG Pro	GGA Gly	TCG Ser	GTC Val	ACC Thr 365	GTG Val	CCA Pro	CAC His	1104
CCA Pro	AAC Asn 370	ATC Ile	GAG Glu	GAG Glu	GTG Val	GCC Ala 375	CTG Leu	TCT Ser	AAT Asn	ACT Thr	GGA Gly 380	GAG Glu	ATC Ile	CCC Pro	TTC Phe	1152
TAT Tyr 385	GGC Gly	AAA Lys	GCC Ala	ATC Ile	CCC Pro 390	ATT Ile	GAA Glu	GCC Ala	ATC Ile	AGG Arg 395	GGG Gly	GGA Gly	AGG Arg	CAT His	CTC Leu 400	1200
ATT Ile	TTC Phe	TGT Cys	CAT His	TCC Ser 405	AAG Lys	AAG Lys	AAG Lys	TGC Cys	GAC Asp 410	GAG Glu	CTC Leu	GCC Ala	GCA Ala	AAG Lys 415	CTG Leu	1248
TCA Ser	GGC Gly	CTC Leu	GGA Gly 420	ATC Ile	AAC Asn	GCT Ala	GTG Val	GCG Ala 425	TAT Tyr	TAC Tyr	CGG Arg	GGG Gly	CTC Leu 430	GAT Asp	GTG Val	1296
TCC Ser	GTC Val	ATA Ile 435	CCA Pro	ACT Thr	ATC Ile	GGA Gly	GAC Asp 440	GTC Val	GTT Val	GTC Val	GTG Val	GCA Ala 445	ACA Thr	GAC Asp	GCT Ala	1344
CTG Leu	ATG Met 450	ACG Thr	GGC Gly	TAT Tyr	ACG Thr	GGC Gly 455	GAC Asp	TTT Phe	GAC Asp	TCA (Ser	GTG Val 460	ATC Ile	GAC Asp	TGT Cys	AAC Asn	1392
ACA Thr 465	TGT Cys	GTC Val	ACC Thr	Gln	ACA Thr 470	GTC (GAC Asp	TTC Phe	Ser	TTG (Leu 475	GAT Asp	CCC Pro	ACC Thr	TTC Phe	ACC Thr 480	1440

ATT Ile	GAG Glu	ACC Thr	ACG Thr	ACC Thi 485	· Val	G CCT	CAZ Glr	A GAC	GCA Ala 490	val	TCG Ser	CGC Arg	TCG Ser	CAC Glr 49!	G CGG n Arg		1488
Arg	GIY	Arg	500	Gly	7 Arg	, Gly	Arg	Arg 505	g Gly	' Il∈	Yyr	Arg	Phe 510	· Val	ACT Thr		1536
PIO	GIĀ	515	Arg	Pro	Ser	. GIĀ	520	: Phe	Asp	Ser	Ser	Val 525	Leu	Суя	GAG Glu		1584
TGC Cys	ТАТ Туг 530	GAC Asp	GCG Ala	GGC Gly	TGT Cys	GCT Ala 535	Trp	TAC Tyr	GAG Glu	CTC Leu	ACC Thr 540	Pro	GCC Ala	GAG Glu	ACC Thr	•	1632
TCG Ser 545	GTT Val	AGG Arg	TTG Leu	CGG Arg	GCC Ala 550	TAC Tyr	CTG Leu	AAC Asn	ACA Thr	CCA Pro 555	GGG Gly	TTG Leu	CCC Pro	GTT Val	TGC Cys 560		1680
CAG Gln	GAC Asp	CAC His	CTG Leu	GAG Glu 565	TTC Phe	TGG Trp	GAG Glu	AGT Ser	GTC Val 570	TTC Phe	ACA Thr	GGC Gly	CTC Leu	ACC Thr 575	CAT His		1728
ATA Ile	GAT Asp	GCA Ala	CAC His 580	TTC Phe	TTG Leu	TCC Ser	CAG Gln	ACC Thr 585	AAG Lys	CAG Gln	GCA Ala	GGA Gly	GAC Asp 590	AAC Asn	TTC Phe		1776
CCC Pro	TAC Tyr	CTG Leu 595	GTA Val	GCA Ala	TAC Tyr	CAA Gln	GCC Ala 600	ACG Thr	GTG Val	TGC Cys	GCC Ala	AGG Arg 605	GCT Ala	CAG Gln	GCC Ala		1824
CCA Pro	CCT Pro 610	CCA Pro	TCA Ser	TGG Trp	GAT Asp	CAA Gln 615	ATG Met	TGG Trp	AAG Lys	TGT Cys	CTC Leu 620	ATA Ile	CGG Arg	CTG Leu	AAA Lys		1872
CCT Pro 625	ACG Thr	CTG Leu	CAC His	GGG Gly	CCA Pro 630	ACA Thr	CCC Pro	TTG Leu	CTG Leu	TAC Tyr 635	AGG Arg	CTG Leu	GGA Gly	GCC Ala	GTC Val 640		1920
CAA Gln	AAT Asn	GAG Glu	Val	ACC Thr 645	CTC Leu	ACC Thr	CAC His	CCC Pro	ATA Ile 650	ACC Thr	AAA Lys	TAC . Tyr	ATC . Ile	ATG Met 655	GCA Ala		1968
TGC . Cys :	ATG ' Met	TCG Ser	GCT (Ala 660	GAC Asp	CTG Leu	GAG (Glu	GTC Val	GTC . Val 665	ACT								1998

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1998 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1997

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His	Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	Ile	TTA. Leu	96
TC T Ser	GGT Gly	AGT Ser 35	GGT Gly	AGT Ser	ATC Ile	ACG Thr	GCC Ala 40	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 45	CGG Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	TGC Cys	AAG Lys	ATC Ile	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	ACT Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	GCG Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly 175	GGT Gly	528

Pro	A CTO	G CTO	TGC Cys 180	Pro	TCC Sei	GGC Gl ₂	G CAC / His	GCT Ala 18!	a Val	GGC Gly	C ATO	TTC Phe	C CGG Arg 190	g Ala	GCC A Ala	576
GTA Val	A TGC Cys	C ACC Thr 195	Arg	GGC Gly	GTT Val	GCG Ala	AAG Lys 200	Ala	G GTG	GAC . Asr	TTT Phe	GTG Val	l Pro	GTA Val	GAG LGlu	624
TCC Ser	Met 210	: Glu	ACT Thr	ACT Thr	ATG Met	CGG Arg 215	, Ser	CCG	GTC Val	TTC Phe	ACG Thr	Asp	AAC Asr	TCA Sei	TCC Ser	672
CCC Pro 225	Pro	GCC Ala	GTA Val	CCG	CAG Gln 230	Ser	TTT Phe	CAA Gln	GTG Val	GCC Ala 235	His	CTA Leu	CAC His	GCT Ala	CCC Pro 240	. 720
ACT Thr	GGC Gly	AGC Ser	GGC Gly	AAG Lys 245	Ser	ACT Thr	AAA Lys	GTG Val	CCG Pro 250	Ala	GCA Ala	TAT Tyr	GCA Ala	GCC Ala 255	CAA Gln	768
GGG Gly	TAC Tyr	AAG Lys	GTG Val 260	CTC Leu	GTC Val	CTC Leu	AAT Asn	CCG Pro 265	Ser	GTT Val	GCC Ala	GCT Ala	ACC Thr 270	Leu	GGG Gly	816
TTT Phe	GGG Gly	GCG Ala 275	TAT Tyr	ATG Met	TCT Ser	AAG Lys	GCA Ala 280	CAC His	GGT Gly	ATT Ile	GAC Asp	CCC Pro 285	Asn	ATC Ile	AGA Arg	864
ACT Thr	GGG Gly 290	GTA Val	AGG Arg	ACC Thr	ATT Ile	ACC Thr 295	ACA Thr	GGC Gly	GCC Ala	CCC Pro	GTC Val 300	ACA Thr	TAC Tyr	TCT Ser	ACC Thr	912
ТАТ Туг 305	GGC Gly	AAG Lys	TTT Phe	CTT Leu	GCC Ala 310	GAT Asp	GGT Gly	GGT Gly	TGC Cys	TCT Ser 315	GGG Gly	GGC Gly	GCT Ala	TAT Tyr	GAC Asp 320	960
ATC Ile	ATA Ile	ATA Ile	TGT Cys	GAT Asp 325	GAG Glu	TGC Cys	CAT His	TCA Ser	ACT Thr 330	Asp	TCG Ser	ACT Thr	ACA Thr	ATC Ile 335	TTG Leu	1008
GGC Gly	ATC Ile	GGC Gly	ACA Thr 340	GTC Val	CTG Leu	GAC Asp	CAA Gln	GCG Ala 345	GAG Glu	ACG Thr	GCT Ala	GGA Gly	GCG Ala 350	CGG Arg	CTT Leu	1056
GTC Val	GTG Val	CTC Leu 355	GCC Ala	ACC Thr	GCT Ala	ACG Thr	CCT Pro 360	CCG Pro	GGA Gly	TCG Ser	GTC Val	ACC Thr 365	GTG Val	CCA Pro	CAC His	1104
CCA Pro	AAC Asn 370	ATC Ile	GAG Glu	GAG Glu	GTG Val	GCC Ala 375	CTG Leu	TCT Ser	AAT Asn	ACT Thr	GGA Gly 380	GAG Glu	ATC Ile	CCC Pro	TTC Phe	1152
TAT Tyr 385	GGC Gly	AAA Lys	GCC . Ala	ATC Ile	CCC Pro 390	ATT Ile	GAA (Glu	GCC Ala	Ile	AGG Arg 395	GGG Gly	GGA Gly	AGG Arg	CAT His	CTC Leu 400	1200
ATT Ile	TTC Phe	TGT Cys	CAT His	TCC Ser	AAG Lys	AAG . Lys	AAG ' Lys '	TGC Cys	GAC (GAG Glu	CTC Leu	GCC Ala	GCA Ala	AAG Lys	CTG Leu	1248

405 410 415 TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG 1296 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT 1344 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala 435 440 CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC 1392 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC 1440 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 470 ATT GAG ACG ACG GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG 1488 Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT 1536 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG 1584 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC 1632 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC 1680 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT 1728 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC 1776 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC 1824 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala 595 600 CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA 1872 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys 615 CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC 1920 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val 630 635

CA/ Glr	A AAT n Asr	GAC Glu	G GTO	C ACC L Thr 645	Leu	ACC Thr	CAC His	CCC Pro	ATA 116 650	Thi	AAA Lys	TAC	ATC	ATG Met 655	GCA Ala	1968
	ATC Met			a Asp					1	1						1998
(2)	INF	ORMA	TION	FOR	SEQ	ID 1	NO:10	08:								
	(:		(A) 1 (B) ' (C) :	LENG: TYPE STRAI	rh: : : nu« NDEDI	ACTE 1998 cleic NESS:	base c ac: : sir	e pa: id	irs							
	(ii	_) M(OLEC	JLE 7	TYPE	: cDI	AI									
	(i)			NAME,		: CDS		5								
	(xi) SE	QUEN	CE D	ESCR	IPTI.	ON:	SEQ	ID N	10:10	8					
ATG Met 1	GGC Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His	AGC Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	CCG Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GGT Gly	TCT Ser	GTT Val	GTT Val 25	ATT Ile	GTT Val	GGT Gly	AGA Arg	ATT Ile 30	Ile	TTA Leu	96
TCT Ser	GGT Gly	AGT Ser 35	GGT Gly	Ser	Ile	ACG Thr	Ala	Tyr	Ser	Gln	Gln	ACG Thr 45	Arg	GGC Gly	CTA Leu	144
CTT Leu	GGT Gly 50	TGC Cys	ATC Ile	AAG Lys	ACT Thr	AGC Ser 55	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 60	AAG Lys	AAC Asn	CAG Gln	GTC Val	192
GAG Glu 65	GGA Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr	ACT Thr	AAT Asn	336

GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC

384

Val	. Asr	o Glr	n Asr) Lei	ı Val	Glv	7 Tr	. clr	. 71-	D To	Dana	- 01			g Ser	
	_	115	,		- • • • •	. 017	120		1 Alc	, PLC	PIC	12		a Ar	g Ser	
TTG Leu	ACA Thr 130	Pro	TGC Cys	ACC Thr	TGI Cys	GGC Gly 135	Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	: Le	GTC 1 Val	ACC Thi	AGA Arg	432
CAT His 145	Ala	GAC Asp	GTC Val	ATT	CCG Pro 150	Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	' Asp	AGT Ser	' AGG	GGG GGG	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC	AGG Arg 165	Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg	Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	Pro	GTA Val	GAG Glu	624
TCC Ser	ATG Met 210	GAA Glu	ACT Thr	ACT Thr	ATG Met	CGG Arg 215	TCT Ser	CCG Pro	GTC Val	TTC Phe	ACG Thr 220	Asp	AAC Asn	TCA Ser	TCC Ser	. 672
CCC Pro 225	CCG Pro	GCC Ala	GTA Val	CCG Pro	CAG Gln 230	TCA Ser	TTT Phe	CAA Gln	GTG Val	GCC Ala 235	CAC His	CTA Leu	CAC His	GCT Ala	CCC Pro 240	720
ACT Thr	GGC Gly	AGC Ser	GGC Gly	AAG Lys 245	AGT Ser	ACT Thr	AAA Lys	GTG Val	CCG Pro 250	GCT Ala	GCA Ala	TAT Tyr	GCA Ala	GCC Ala 255	CAA Gln	768
GGG Gly	TAC Tyr	AAG Lys	GTG Val 260	CTC Leu	GTC Val	CTC Leu	AAT Asn	CCG Pro 265	TCC Ser	GTT Val	GCC Ala	GCT Ala	ACC Thr 270	TTA Leu	GGG Gly	816
TTT Phe	GGG Gly	GCG Ala 275	TAT Tyr	ATG Met	TCT Ser	AAG Lys	GCA Ala 280	CAC His	GGT Gly	ATT Ile	GAC Asp	CCC Pro 285	AAC Asn	ATC Ile	AGA Arg	864
ACT Thr	GGG Gly 290	GTA Val	AGG Arg	ACC Thr	ATT Ile	ACC Thr 295	ACA Thr	GGC Gly	GCC Ala	CCC Pro	GTC Val 300	ACA Thr	TAC Tyr	TCT Ser	ACC Thr	912
тат Туг 305	GGC Gly	AAG Lys	TTT Phe	CTT Leu	GCC Ala 310	GAT Asp	GGT Gly	GGT Gly	TGC Cys	TCT Ser 315	GGG Gly	GGC Gly	GCT Ala	TAT Tyr	GAC Asp 320	960
ATC Ile	ATA Ile	ATA Ile	TGT Cys	GAT Asp 325	GAG Glu	TGC Cys	CAT His	TCA Ser	ACT Thr 330	GAC Asp	TCG Ser	ACT Thr	ACA Thr	ATC Ile 335	TTG Leu	1008
GGC Gly	ATC Ile	Gly	ACA Thr 340	GTC Val	CTG Leu	GAC Asp	CAA Gln	GCG Ala 345	GAG Glu	ACG Thr	GCT Ala	GGA Gly	GCG Ala 350	CGG Arg	CTT Leu	1056

		CTC Leu 355														110	4
		ATC Ile														115	2
		AAA Lys														120	0
		TGT Cys														124	8
		CTC Leu														129	6
		АТА Ile 435														134	4
		ACG Thr														139	2
		GTC Val														144	0
		ACG Thr														148	8
		AGG Arg			Arg		Arg	Arg	Gly	Ile		Arg	Phe	Val		153	6
		GAA Glu 515														158	4
		GAC Asp														163	2
		AGG Arg														168	0
		CAC His														172	8
ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	177	6

Il∈	Asp	Ala	His 580	Phe	Leu	Ser	Gln	Thr 585		Gln	Ala	Gly	Asp 590		Phe	
CCC Pro	TAC Tyr	CTG Leu 595	GTA Val	GCA Ala	TAC Tyr	CAA Gln	GCC Ala 600	ACG Thr	GTG Val	TGC Cys	GCC Ala	AGG Arg 605	Ala	CAG Gln	GCC Ala	1824
CCA Pro	CCT Pro 610	CCA Pro	TCA Ser	TGG Trp	GAT Asp	CAA Gln 615	ATG Met	TGG Trp	AAG Lys	TGT Cys	CTC Leu 620	Ile	CGG Arg	CTG Leu	AAA Lys	1872
CCT Pro 625	ACG Thr	CTG Leu	CAC His	GGG Gly	CCA Pro 630	ACA Thr	CCC Pro	TTG Leu	CTG Leu	TAC Tyr 635	AGG Arg	CTG Leu	GGA Gly	GCC Ala	GTC Val 640	1920
CAA Gln	AAT Asn	GAG Glu	GTC Val	ACC Thr 645	CTC Leu	ACC Thr	CAC His	CCC Pro	ATA Ile 650	ACC Thr	AAA Lys	TAC Tyr	ATC Ile	ATG Met 655	GCA Ala	1968
	ATG Met														•	1998
	(ii (ix (ix) SE ((((((((QUENA) L. B) T C) S D) T LECUT ATUR A) N. B) L ATUR A) N. B) L B) L	CE C. ENGTI YPE: TRANI OPOL E: AME/I OCATI	HARAMENT IN THE PROPERTY IN T	CTER: 998 } leic ESS: line CDN CDS 11	ISTIC Dase acic singear A	CS: pai d gle		D:109) :					
	GGC Gly															48
CGC Arg	GGC Gly	AGC Ser	CAT . His	ATG (GGT '	TCT (Ser '	GTT (GTT . Val 25	ATT (GTT (Val	GGT Gly	AGA Arg	ATT Ile 30	ATT '	TTĄ Leu	96
	GGT Gly															144

CTT Leu	GGT Gly 50	Суз	AAG Lys	AAG Lys	ACT Thr	AGC Ser 55	Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp	Lys	AAC Asr	CAG Glr	GTC Val	192
GAG Glu 65	Gly	GAG Glu	GTT Val	CAG Gln	GTG Val 70	Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 75	Gln	TCC Ser	TTC Phe	CTG Lev	GCG Ala 80	240
ACC Thr	TGC Cys	GTC Val	AAC Asn	GGC Gly 85	Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 90	Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 95	TCA Ser	288
AAG Lys	ACC Thr	TTA Leu	GCC Ala 100	GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 105	Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 110	Thr	AAT Asn	336
GTG Val	GAC Asp	CAG Gln 115	GAC Asp	CTC Leu	GTC Val	GGC Gly	TGG Trp 120	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 125	Ala	CGT Arg	TCC Ser	384
TTG Leu	ACA Thr 130	CCA Pro	TGC Cys	ACC Thr	TGT Cys	GGC Gly 135	AGC Ser	TCA Ser	GAC Asp	CTT Leu	TAC Tyr 140	TTG Leu	GTC Val	ACG Thr	AGA Arg	432
CAT His 145	GCT Ala	GAC Asp	GTC Val	ATT Ile	CCG Pro 150	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 155	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 160	480
CTG Leu	CTC Leu	TCC Ser	CCC Pro	AGG Arg 165	CCT Pro	GTC Val	TCC Ser	TAC Tyr	TTG Leu 170	AAG Lys	GGC Gly	TCT Ser	GCT Ala	GGT Gly 175	GGT Gly	528
CCA Pro	CTG Leu	CTC Leu	TGC Cys 180	CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 185	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 190	GCT Ala	GCC Ala	576
GTA Val	TGC Cys	ACC Thr 195	CGG Arg	GGG Gly	GTT Val	GCG Ala	AAG Lys 200	GCG Ala	GTG Val	GAC Asp	TTT Phe	GTG Val 205	CCC Pro	GTA Val	GAG Glu	624
TCC Ser	ATG Met 210	GAA Glu	ACT Thr	ACT Thr	ATG Met	CGG Arg 215	TCT Ser	CCG Pro	GTC Val	TTC Phe	ACG Thr 220	GAC Asp	AAC Asn	TCA Ser	TCC Ser	672
CCC Pro 225	CCG Pro	GCC Ala	GTA Val	CCG Pro	CAG Gln 230	TCA Ser	TTT Phe	CAA Gln	GTG Val	GCC Ala 235	CAC His	CTA Leu	CAC His	GCT Ala	CCC Pro 240	720
ACT Thr	GGC Gly	AGC Ser	GGC Gly	AAG Lys 245	AGT Ser	ACT Thr	AAA Lys	GTG Val	CCG Pro 250	GCT Ala	GCA Ala	TAT Tyr	GCA Ala	GCC Ala 255	CAA Gln	768
GGG Gly	TAC Tyr	AAG Lys	GTG Val 260	CTC Leu	GTC Val	CTC Leu	AAT Asn	CCG Pro 265	TCC Ser	GTT Val	GCC Ala	GCT Ala	ACC Thr 270	TTA Leu	GGG Gly	816
TTT Phe	GGG Gly	GCG Ala	TAT Tyr	ATG Met	TCT Ser	AAG Lys	GCA Ala	CAC His	GGT Gly	ATT Ile	GAC Asp	CCC Pro	AAC Asn	ATC Ile	AGA Arg	864

275 280 285 ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC 912 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC 960 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 315 ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG 1008 Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGT 1056 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC-1104 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 360 CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC 1152 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 375 380 TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC 1200 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 ATT TTC TGT CAT TCC AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG 1248 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG 1296 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT 1344 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC 1392 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC 1440 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 470 475 ATT GAG ACG ACG GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG 1488 Ile Glu Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT 1536 Arg Gly Arg Thr Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510

CCC Pro	G GGA	GAA Glu 515	ı Arg	Pro	TCG Ser	GGC Gly	ATG Met	: Ph∈	GAT Asp	TCC Ser	TCG Ser	GTC Val	Leu	TGT Cys	GAG Glu	1584
TGC Cys	TAT Tyr 530	' Asp	GCG Ala	GGC Gly	TGT Cys	GCT Ala 535	Trp	TAC Tyr	GAG Glu	CTC Leu	ACC Thr	Pro	GCC Ala	GAG Glu	ACC Thr	1632
TCG Ser 545	Val	AGG Arg	TTG Leu	CGG Arg	GCC Ala 550	TAC Tyr	CTG Leu	AAC Asn	ACA Thr	CCA Pro 555	GGG Gly	TTG Leu	CCC Pro	GTT Val	TGC Cys 560	1680
CAG Gln	GAC Asp	CAC His	CTG Leu	GAG Glu 565	TTC Phe	TGG Trp	GAG Glu	AGT Ser	GTC Val 570	TTC Phe	ACA Thr	GGC Gly	CTC Leu	ACC Thr 575	CAT His	1728
ATA Ile	GAT Asp	GCA Ala	CAC His 580	TTC Phe	TTG Leu	TCC Ser	CAG Gln	ACC Thr 585	AAG Lys	CAG Gln	GCA Ala	GGA Gly	GAC Asp 590	AAC Asn	TTC Phe	1776
CCC Pro	TAC Tyr	CTG Leu 595	GTA Val	GCA Ala	TAC Tyr	CAA Gln	GCC Ala 600	ACG Thr	GTG Val	TGC Cys	GCC Ala	AGG Arg 605	GCT Ala	CAG Gln	GCC Ala	1824
CCA Pro	CCT Pro 610	CCA Pro	TCA Ser	TGG Trp	GAT Asp	CAA Gln 615	ATG Met	TGG Trp	AAG Lys	TGT Cys	CTC Leu 620	ATA Ile	CGG Arg	CTG Leu	AAA Lys	1872
CCT Pro 625	ACG Thr	CTG Leu	CAC His	GGG Gly	CCA Pro 630	ACA Thr	CCC Pro	TTG Leu	CTG Leu	TAC Tyr 635	AGG Arg	CTG Leu	GGA Gly	GCC Ala	GTC Val 640	1920
CAA Gln	AAT Asn	GAG Glu	GTC Val	ACC Thr 645	CTC Leu	ACC Thr	CAC His	CCC Pro	ATA Ile 650	ACC Thr	AAA Lys	TAC Tyr	ATC Ile	ATG Met 655	GCA Ala	1968
TGC Cys	ATG Met	TCG Ser	GCT Ala 660	GAC Asp	CTG Leu	GAG (Glu	GTC (GTC . Val 665	ACT							1998

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2016 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

мет	G GGG G Gl ₂	C AG	C AGO	C CAT c His	His	CAT His	CA:	r CAn	CAC His	s Se	C AGO	GGC Gly	CTC / Le	ม Va	G CCG 1 Pro 5 °	48
CGC Arg	GG(C AGO	C CAT His 20	s Met	GCT Ala	TAC Tyr	TC1	CTC Let 25	ı Thi	ACG Thi	GGT	TCT Ser	GTT Val	l Va	r ATT l Ile	96
GTT Val	Gly	AGA Arg 3!	1 ITE	TATT	TTA Leu	TCT Ser	GGT Gly	/ Ser	GGT	AGT Ser	TATC	ACG Thr	A1a	TAC	TCC Ser	144
CAA Gln	CAG Glr 50	נמיזי ו	G CGG Arg	GGC Gly	CTA Leu	CTT Leu 55	Gly	' TGC	ATC	ATC : Ile	ACT Thr	Ser	CTT Leu	ACA Thi	GGC Gly	192
CGG Arg 65	Asp	AAC Lys	AAC Asn	CAG Gln	GTC Val 70	GAG Glu	GGA Gly	GAG Glu	GTT Val	CAG Gln 75	Val	GTT Val	TCC Ser	ACC Thr	GCA Ala 80	240
ACA Thr	CAA Gln	TCC Ser	TTC Phe	CTG Leu 85	GCG Ala	ACC Thr	TGC Cys	GTC Val	AAC Asn 90	Gly	GTG Val	TGT Cys	TGG Trp	ACC Thr 95	Val	288
TAC Tyr	CAT His	GGT Gly	GCT Ala 100	GGC Gly	TCA Ser	AAG Lys	ACC Thr	TTA Leu 105	GCC Ala	GGC Gly	CCA Pro	AAG Lys	GGG Gly 110	CCA Pro	ATC Ile	336
ACC Thr	CAG Gln	ATG Met 115	TAC Tyr	ACT Thr	AAT Asn	GTG Val	GAC Asp 120	CAG Gln	GAC Asp	CTC Leu	GTC Val	GGC Gly 125	TGG Trp	CAG Gln	GCG Ala	384
CCC Pro	CCC Pro 130	GGG Gly	GCG Ala	CGT Arg	TCC Ser	TTG Leu 135	ACA Thr	CCA Pro	TGC Cys	ACC Thr	TGT Cys 140	GGC Gly	AGC Ser	TCA Ser	GAC Asp	432
CTT Leu 145	TAC Tyr	TTG Leu	GTC Val	ACG Thr	AGA Arg 150	CAT His	GCT Ala	GAC Asp	GTC Val	ATT Ile 155	CCG Pro	GTG Val	CGC Arg	CGG Arg	CGG Arg 160	480
GGC Gly	GAC Asp	AGT Ser	AGG Arg	GGG Gly 165	AGC Ser	CTG Leu	CTC Leu	TCC Ser	CCC Pro 170	AGG Arg	CCT Pro	GTC Val	TCC Ser	TAC Tyr 175	TTG Leu	528
AAG Lys	GGC Gly	TCT Ser	TCG Ser 180	GGT (GGT Gly	CCA Pro	CTG Leu	CTC Leu 185	TGC Cys	CCT Pro	TCG Ser	GGG Gly	CAC His 190	GCT Ala	GTG Val	576
GGC Gly	ATC Ile	TTC Phe 195	CGG Arg	GCT (Ala .	GCC Ala	GTA (TGC Cys 200	ACC Thr	CGG Arg	GGG Gly	GTT Val	GCG Ala 205	AAG Lys	GCG Ala	GTG Val	624
Asp	TTT Phe 210	GTG Val	CCC Pro	GTA (Val (Glu	TCC Z Ser 1 215	ATG Met	GAA . Glu	ACT Thr	ACT . Thr	ATG Met 220	CGG Arg	TCT Ser	CCG Pro	GTC Val	672

TTC Phe 225	Thr	G GAC Asp	AAC Asr	TCA Ser	TCC Ser 230	Pro	CCG Pro	GCC Ala	C GTA u Val	CCG Pro 235	Glr	TCA Sei	TTT Phe	CAA Glr	GTG Val 240	720
GCC Ala	CAC His	CTA Leu	CAC His	GCT Ala 245	Pro	ACT Thr	GGC Gly	AGC Ser	GGC G1 _y 250	Lys	AGT Ser	ACT Thr	' AAA : Lys	GTG Val	CCG Pro	768
GCT Ala	GCA Ala	TAT Tyr	GCA Ala 260	Ala	CAA Gln	GGG Gly	TAC Tyr	AAG Lys 265	Val	CTC Leu	GTC Val	CTC Lev	AAT Asn 270	Pro	TCC Ser	816
GTT Val	GCC Ala	GCT Ala 275	ACC Thr	TTA Leu	GGG Gly	TTT Phe	GGG Gly 280	GCG Ala	TAT Tyr	ATG Met	TCT Ser	AAG Lys 285	Ala	CAC His	GGT Gly	. 864
ATT Ile	GAC Asp 290	CCC Pro	AAC Asn	ATC Ile	AGA Arg	ACT Thr 295	GGG Gly	GTA Val	AGG Arg	ACC Thr	ATT Ile 300	Thr	ACA Thr	GGC Gly	GCC Ala	912
CCC Pro 305	GTC Val	ACA Thr	TAC Tyr	TCT	ACC Thr 310	TAT Tyr	GGC Gly	AAG Lys	TTT Phe	CTT Leu 315	GCC Ala	GAT Asp	GGT Gly	GGT Gly	TGC Cys 320	960
TCT Ser	GGG Gly	GGC Gly	GCT Ala	ТАТ Туг 325	GAC Asp	ATC Ile	ATA Ile	ATA Ile	TGT Cys 330	GAT Asp	GAG Glu	TGC Cys	CAT	TCA Ser 335	ACT Thr	1008
GAC Asp	TCG Ser	ACT Thr	ACA Thr 340	ATC Ile	TTG Leu	GGC Gly	ATC Ile	GGC Gly 345	ACA Thr	GTC Val	CTG Leu	GAC Asp	CAA Gln 350	GCG Ala	GAG Glu	1056
ACG Thr	GCT Ala	GGA Gly 355	GCG Ala	CGG Arg	CTT Leu	GTC Val	GTG Val 360	CTC Leu	GCC Ala	ACC Thr	GCT Ala	ACG Thr 365	CCT Pro	CCG Pro	GGA Gly	1104
TCG Ser	GTC Val 370	ACC Thr	GTG Val	CCA Pro	CAC His	CCA Pro 375	AAC Asn	ATC Ile	GAG Glu	GAG Glu	GTG Val 380	GCC Ala	CTG Leu	TCT Ser	AAT Asn	1152
ACT Thr 385	GGA Gly	GAG Glu	ATC Ile	CCC Pro	TTC Phe 390	TAT Tyr	GGC Gly	AAA Lys	GCC Ala	ATC Ile 395	CCC Pro	ATT Ile	GAA Glu	GCC Ala	ATC Ile 400	1200
AGG Arg	GGG Gly	GGA Gly	AGG Arg	CAT His 405	CTC Leu	ATT Ile	TTC Phe	TGT Cys	CAT His 410	TCC Ser	AAG Lys	AAG Lys	AAG Lys	TGC Cys 415	GAC Asp	1248
GAG Glu	CTC Leu	GCC Ala	GCA Ala 420	AAG Lys	CTG Leu	TCA Ser	GGC Gly	CTC Leu 425	GGA Gly	ATC Ile	AAC Asn	GCT Ala	GTG Val 430	GCG Ala	тат ту <u>г</u>	1296
TAC Tyr	CGG Arg	GGG Gly 435	CTC Leu	GAT Asp	GTG Val	TCC Ser	GTC Val 440	ATA Ile	CCA Pro	ACT Thr	ATC Ile	GGA Gly 445	GAC Asp	GTC Val	GTT Val	1344
GTC	GTG	GCA	ACA	GAC	GCT	CTG .	ATG .	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	1392

Va]	. Va] 45(Ala	Thr	Ası	o Ala	Leu 455	Met	: Thi	Gly	у Туг	Thr 460		⁄ Asp	Ph∈	e Asp	
TCA Ser 465	Val	ATC	GAC Asp	TGT Cys	AAC Asn 470	Thr	TGT Cys	GTC Val	ACC Thr	CAG Glr 475	Thr	GTC Val	GAC Asp	TTC Phe	AGC Ser 480	1440
TTG Leu	GAT Asp	CCC Pro	ACC Thr	TTC Phe 485	Thr	ATT Ile	GAG Glu	ACG Thr	ACG Thr 490	Thr	GTG Val	CCT Pro	CAA Gln	GAC Asp 495	GCA Ala	1488
GTG Val	TCG Ser	CGC Arg	TCG Ser 500	CAG Gln	CGG Arg	CGG Arg	GGT Gly	AGG Arg 505	Thr	GGC Gly	AGG Arg	GGT Gly	AGG Arg 510	AGA Arg	GGC Gly	1536
ATC Ile	TAC Tyr	AGG Arg 515	TTT Phe	GTG Val	ACT Thr	CCG Pro	GGA Gly 520	Glu	CGG Arg	CCC Pro	TCG Ser	GGC Gly 525	Met	TTC Phe	GAT Asp	1584
TCC Ser	TCG Ser 530	GTC Val	CTG Leu	TGT Cys	GAG Glu	TGC Cys 535	TAT Tyr	GAC Asp	GCG Ala	GGC Gly	TGT Cys 540	Ala	TGG Trp	TAC Tyr	GAG Glu	1632
CTC Leu 545	ACC Thr	CCC Pro	GCC Ala	GAG Glu	ACC Thr 550	TCG Ser	GTT Val	AGG Arg	TTG Leu	CGG Arg 555	GCC Ala	TAC Tyr	CTG Leu	AAC Asn	ACA Thr 560	1680
CCA Pro	GGG Gly	TTG Leu	CCC Pro	GTT Val 565	TGC Cys	CAG Gln	GAC Asp	CAC His	CTG Leu 570	GAG Glu	TTC Phe	TGG Trp	GAG Glu	AGT Ser 575	GTC Val	1728
TTC Phe	ACA Thr	GGC Gly	CTC Leu 580	ACC Thr	CAT His	ATA Ile	GAT Asp	GCA Ala 585	CAC His	TTC Phe	TTG Leu	TCC Ser	CAG Gln 590	ACC Thr	AAG Lys	1776
CAG Gln	GCA Ala	GGA Gly 595	GAC Asp	AAC Asn	TTC Phe	CCC Pro	TAC Tyr 600	CTG Leu	GTA Val	GCA Ala	TAC Tyr	CAA Gln 605	GCC Ala	ACG Thr	GTG Val	1824
TGC Cys	GCC Ala 610	AGG Arg	GCT Ala	CAG Gln	GCC Ala	CCA Pro 615	CCT Pro	CCA Pro	TCA Ser	TGG Trp	GAT Asp 620	CAA Gln	ATG Met	TGG Trp	AAG Lys	1872
TGT Cys 625	CTC Leu	ATA Ile	CGG Arg	CTG Leu	AAA Lys 630	CCT Pro	ACG Thr	CTG Leu	CAC His	GGG Gly 635	CCA Pro	ACA Thr	CCC Pro	TTG Leu	CTG Leu 640	1920
TAC Tyr	AGG Arg	CTG Leu	Gly	GCC Ala 645	GTC Val	CAA Gln	AAT Asn	GAG Glu	GTC Val 650	ACC Thr	CTC Leu	ACC Thr	CAC His	CCC Pro 655	ATA Ile	1968
ACC Thr	AAA Lys	Tyr	ATC . Ile 660	ATG Met	GCA Ala	TGC . Cys	ATG Met	TCG Ser 665	GCT Ala	GAC Asp	CTG Leu	GAG (GTC (Val 670	GTC Val		2013
ACT																2016

(2) INFORMATION FOR SEQ ID NO:111:

(i)	SEQUENCE	CHARACTERISTICS:
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- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATG Met 1	Gly	AGC Ser	AGC Ser	CAT His 5	CAT His	CAT His	CAT His	CAT His	CAC His	Ser	AGC Ser	GGC Gly	CTG Leu	GTG Val 15	Pro	48
CGC Arg	GGC Gly	AGC Ser	CAT His 20	ATG Met	GCT Ala	TAC Tyr	TCT Ser	CTG Leu 25	ACT Thr	ACG Thr	GGT Gly	TCT Ser	GTT Val 30	GTT Val	ATT Ile	96
GTT Val	GGT Gly	AGA Arg 35	ATT Ile	ATT Ile	TTA Leu	TCT Ser	GGT Gly 40	AGT Ser	GGT Gly	AGT Ser	ATC Ile	ACG Thr 45	GCC Ala	TAC Tyr	TCC Ser	144
CAA Gln	CAG Gln 50	ACG Thr	CGG Arg	GGC Gly	CTA Leu	CTT Leu 55	GGT Gly	TGC Cys	ATC Ile	ATC Ile	ACT Thr 60	AGC Ser	CTT Leu	ACA Thr	GGC Gly	192
CGG Arg 65	GAC Asp	AAG Lys	AAC Asn	CAG Gln	GTC Val 70	GAG Glu	GGA Gly	GAG Glu	GTT Val	CAG Gln 75	GTG Val	GTT Val	TCC Ser	ACC Thr	GCA Ala 80	240
ACA Thr	CAA Gln	TCC Ser	TTC Phe	CTG Leu 85	GCG Ala	ACC Thr	TGC Cys	GTC Val	AAC Asn 90	GGC Gly	GTG Val	TGT Cys	TGG Trp	ACC Thr 95	GTT Val	288
TAC Tyr	CAT His	GGT Gly	GCT Ala 100	GGC Gly	TCA Ser	AAG Lys	ACC Thr	TTA Leu 105	GCC Ala	GGC Gly	CCA Pro	AAG Lys	GGG Gly 110	CCA Pro	ATC Ile	336
ACC Thr	CAG Gln	ATG Met 115	TAC Tyr	ACT Thr	AAT Asn	GTG Val	GAC Asp 120	CAG Gln	GAC Asp	CTC Leu	GTC Val	GGC Gly 125	TGG Trp	CAG Gln	GCG Ala	384
CCC Pro	CCC Pro 130	GGG Gly	GCG Ala	CGT Arg	TCC Ser	TTG Leu 135	ACA Thr	CCA Pro	TGC Cys	ACC Thr	TGT Cys 140	GGC Gly	AGC Ser	TCA Ser	GAC Asp	432
CTT Leu 145	TAC Tyr	TTG Leu	GTC Val	ACG Thr	AGA Arg 150	CAT His	GCT Ala	GAC Asp	GTC Val	ATT Ile 155	CCG Pro	GTG Val	CGC Arg	CGG Arg	CGG Arg 160	480

GGC Gly	GAC Asp	: AGT Ser	AGG Arg	GGG G1 _y 165	/ Ser	CTG Leu	CTC Leu	TCC Ser	CCC Pro	Arg	CCT Pro	GTC Val	TCC Ser	TAC Tyr 175	TTG Leu		528
AAG Lys	GGC Gly	TCT Ser	GCT Ala 180	. Gly	GGT Gly	CCA Pro	CTG Leu	CTC Leu 185	Cys	CCT Pro	TCG Ser	GGG	CAC His	Ala	GTG Val	7	576
GGC Gly	ATC	TTC Phe 195	CGG Arg	GCT Ala	GCC Ala	GTA Val	TGC Cys 200	Thr	CGG Arg	GGG Gly	GTT Val	GCG Ala 205	Lys	GCG Ala	GTG Val		624
GAC Asp	TTT Phe 210	Val	CCC Pro	GTA Val	GAG Glu	TCC Ser 215	Met	GAA Glu	ACT Thr	ACT Thr	ATG Met 220	Arg	TCT Ser	CCG Pro	GTC Val	٠	672
TTC Phe 225	ACG Thr	GAC Asp	AAC Asn	TCA Ser	TCC Ser 230	CCC Pro	CCG Pro	GCC Ala	GTA Val	CCG Pro 235	CAG Gln	TCA Ser	TTT Phe	CAA Gln	GTG Val 240		720
GCC Ala	CAC His	CTA Leu	CAC His	GCT Ala 245	CCC Pro	ACT Thr	GGC Gly	AGC Ser	GGC Gly 250	AAG Lys	AGT Ser	ACT Thr	AAA Lys	GTG Val 255	CCG Pro		768
GCT Ala	GCA Ala	TAT Tyr	GCA Ala 260	GCC Ala	CAA Gln	GGG Gly	TAC Tyr	AAG Lys 265	GTG Val	CTC Leu	GTC Val	CTC Leu	AAT Asn 270	CCG Pro	TCC Ser		816
GTT Val	GCC Ala	GCT Ala 275	ACC Thr	TTA Leu	GGG Gly	TTT Phe	GGG Gly 280	GCG Ala	TAT Tyr	ATG Met	TCT Ser	AAG Lys 285	GCA Ala	CAC His	GGT Gly		864
ATT Ile	GAC Asp 290	CCC Pro	AAC Asn	ATC Ile	AGA Arg	ACT Thr 295	GGG Gly	GTA Val	AGG Arg	ACC Thr	ATT Ile 300	ACC Thr	ACA Thr	GGC Gly	GCC Ala		912
CCC Pro 305	GTC Val	ACA Thr	TAC Tyr	TCT Ser	ACC Thr 310	\mathtt{Tyr}	Gly	Lys	TTT Phe	Leu	GCC Ala	GAT Asp	GGT Gly	GGT Gly	TGC Cys 320		960
TCT Ser	GGG Gly	GGC Gly	GCT Ala	TAT Tyr 325	GAC Asp	ATC Ile	ATA Ile	ATA Ile	TGT Cys 330	GAT Asp	GAG Glu	TGC Cys	CAT His	TCA Ser 335	ACT Thr		1008
GAC Asp	TCG Ser	ACT Thr	ACA Thr 340	ATC Ile	TTG Leu	GGC Gly	ATC Ile	GGC Gly 345	ACA Thr	GTC Val	CTG Leu	GAC Asp	CAA Gln 350	GCG Ala	GAG Glu		1056
ACG Thr	GCT Ala	GGA Gly 355	GCG Ala	CGG Arg	CTT Leu	GTC Val	GTG Val 360	CTC Leu	GCC Ala	ACC Thr	GCT Ala	ACG Thr 365	CCT Pro	CCG Pro	GGA G1y		1104
TCG Ser	GTC Val 370	ACC Thr	GTG Val	CCA Pro	CAC His	CCA Pro 375	AAC Asn	ATC Ile	GAG Glu	GAG Glu	GTG Val 380	GCC Ala	CTG Leu	TCT Ser	AAT Asn		1152
АСТ	GGA	GAG	ATC	ccc	TTC	TAT	GGC	AAA	GCC	ATC	ccc	ATT	GAA	GCC	ATC		1200

Thr 385	Gly	Glu	Ile	Pro	Phe 390	Tyr	Gly	Lys	Ala	Ile 395	Pro	Ile	Glu	Ala	Ile 400	
					CTC Leu											1248
					CTG Leu											1296
					GTG Val										GTT Val	1344
					GCT Ala											1392
					AAC Asn 470											1440
					ACC Thr											1488
					CGG Arg											1536
					ACT Thr											1584
					GAG Glu											1632
					ACC Thr 550											1680
					TGC Cys											1728
					CAT His											1776
					TTC Phe											1824
					GCC Ala											1872

TGT	CTC	ATA	CGG	CTG	AAA	CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	1920
_	Leu	Ile	Arg	Leu	_	Pro	Thr	Leu	His	_	Pro	Thr	Pro	Leu		
625					630					635					640	
TAC	AGG	CTG	GGA	GCC	GTC	CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	1968
Tyr	Arg	Leu	Gly		Val	Gln	Asn	Glu	Val	Thr	Leu	Thr	His	Pro	Ile	
				645					650					655		
ACC	AAA,	TAC	ATC	ATG	GCA	TGC	ATG	TCG	GCT	GAC	CTG	GAG	GTC	GTC		2013
Thr	Lys	Tyr		Met	Ala	Суѕ	Met	Ser	Ala	Asp	Leu	Glu	Val	Val		
			660					665					670			
ACT															•	2016

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

	GGC															48
_	Gly	Ser	Ser		His	His	His	His		Ser	Ser	Gly	Leu		Pro	
1				5					10					15		
ccc	GGC	700	CAM	7 MC	CCIII	mom.	C III III	amm.	» mm	amm.	COM	707	3 mm	3 MM	mm »	96
						-										90
Arg	Gly	ser		met	GIY	ser	vai		тте	vai	GIA	Arg		тте	ьeu	
			20					25					30			
TICT.	ССТ	CCT	CCM	አጥር	ACC:	ccc	መልር	mcc.	C A A	CAC	A C C	CCC	CCC	Cmx	Cmm.	144
							_		_	-					-	7.4.4
ser	Pro	35	GTY	тте	1111	Ala	_	ser	GIII	GIII	TILL	_	GIY	Leu	Leu	
		33					40					45				
GGT	TGC	ATC	ΑΤС	ΔCΨ	AGC	Cuhuh	ACA	GGC	CGG	GAC	AAG	ממכ	CAG	GTC	GAG	192
	Cys															172
Gry	50	110	110	1111	DCI	55	1111	OLY	AI 9	изр	60	non	CIII	vai	GIG	
	50					33					00					
GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	ACC	240
_	Glu															
65					70					75					80	
TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	288
Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	
_			_		_	_			-		-		-		_	
				85					90					95		

	GCC Ala								336
	GAC Asp 115								384
	TGC Cys								432
	GTC Val								480
	CCC Pro								528
	TGC Cys								576
	CGG Arg 195								624
	ACT Thr			*					648

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..640
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAT	CAC	AGC	AGC	GGC	CTG	GTG	CCG	4	8
Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro		
1				5					10					15			

CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu 20 TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT 144 Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG 192 Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC 240 Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr 75 TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG 288 Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys . 90 ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG 336 Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val 100 GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG 384 Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu 115 ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT 432 Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His 130 135 GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG 480 Ala Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu 150 155 CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA 528 Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro 170 CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA 576 Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val 185 TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC 624 Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser 195 200 205 ATG GAA ACT ACT ATG C GGTCTTGA 648 Met Glu Thr Thr Met 210

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS(B) LOCATION: 1..498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATG Met 1	ATC Ile	ACT Thr	AGC Ser	CTT Leu 5	ACA Thr	GGC Gly	CGG Arg	GAC Asp	AAG Lys 10	AAC Asn	CAG Gln	GTC Val	GAG Glu	GGA Gly 15	GAG Glu	. 48
						GCA Ala										96
						GTT Val										144
						ATC Ile 55										192
						GCG Ala										240
						GAC Asp										288
						CGG Arg										336
						TTG Leu										384
						GTG Val 135										432
						GTG Val										480
	ACT Thr				*											498

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

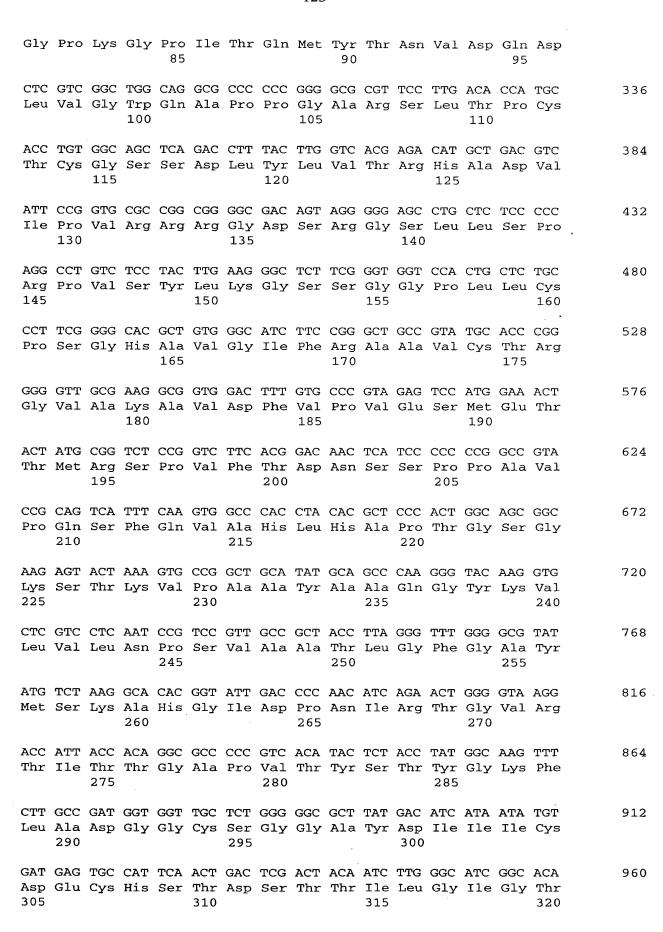
GGC Gly							CCG. Pro	48
GGC Gly								96
GGT Gly								144
TGC Cys 50								192
GAG Glu								240
GTC Val								288
TTA Leu								336
CAG Gln	Leu							384
CCA Pro 130								432
GAC Asp								480

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2007 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATG	CAT	ATG	CAT	CAT	CAT	CAC	CAT	CAT	CTG	GTG	CCG	CGC	GGC	AGC	GCG	48
Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	
1				5					10					15		
CCC	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	CTT	GGT	TGC	AAG	96
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Lys	
			20					25					30	_	_	
ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	GAG	GGA	GAG	GTT	144
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	
		35					40					45				
CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC	192
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	
	50					55					60					
GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC	240
${ t Gly}$	Val	Cys	\mathtt{Trp}	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	
65					70					75					80	
GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC	288



GTC Val	CTG Leu	GAC Asp	CAA Gln	GCG Ala 325	Glu	ACG Thr	GCT Ala	GGA Gly	GCG Ala 330	CGG Arg	CTT Leu	GTC Val	GTG Val	CTC Leu 335	Ala	1008
ACC Thr	GCT Ala	ACG Thr	CCT Pro 340	CCG Pro	GGA Gly	TCG Ser	GTC Val	ACC Thr 345		CCA Pro	CAC His	CCA Pro	AAC Asn 350	Ile	GAG Glu	1056
GAG Glu	GTG Val	GCC Ala 355	CTG Leu	TCT Ser	AAT Asn	ACT Thr	GGA Gly 360	Glu	ATC Ile	CCC Pro	TTC Phe	TAT Tyr 365	Gly	AAA Lys	GCC Ala	1104
							Gly		AGG Arg			Ile				. 1152
									GCA Ala							1200
									CTC Leu 410							1248
									ACA Thr							1296
									GAC Asp							1344
									ACC Thr							1392
			Gln	Asp		Val			TCG Ser		Arg					1440
									TTT Phe 490							1488
									CTG Leu							1536
									GCC Ala							1584
									CCC Pro							1632
GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	СТС	ACC	CAT	АТА	GAT	GCA	CAC	1680

Glu 545	Phe	Trp	Glu	Ser	Val 550	Phe	Thr	Gly	Leu	Thr 555	His	Ile	Asp	Ala	His 560	
												CCC Pro				1728
												CCA Pro				1776
												CCT Pro 605				1824
												CAA Gln				1872
												TGC Cys				1920
												CGA Arg				1968
						CCA Pro										2007

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2007 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..2004
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ATG	CAT	ATG	CAT	CAT	CAT	CAC	CAT	CAT	CTG	GTG	CCG	CGC	GGC	AGC	GCG	48
Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	
1				5					10				-	15		
CCC	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	СТА	СТТ	GGT	TGC	ATC	96

CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile

20 25 30

			CGG Arg						144
			ACA Thr 55			Thr			192
			TAC Tyr						240
			ACC Thr						288
			CCC Pro						336
			CTT Leu						384
			GGC Gly 135						432
			AAG Lys						480
			GGC Gly						528
			GAC Asp						576
			TTC Phe						624
			GCC Ala 215						672
			GCT Ala						720
_			GTT Val						768

ATG Met	TCT Ser	AAG Lys	GCA Ala 260	CAC His	GGT Gly	ATT Ile	GAC Asp	CCC Pro 265	AAC Asn	ATC Ile	AGA Arg	ACT Thr	GGG Gly 270	Val	AGG Arg	816
ACC Thr	ATT Ile	ACC Thr 275	ACA Thr	GGC Gly	GCC Ala	CCC Pro	GTC Val 280	ACA Thr	TAC Tyr	TCT Ser	ACC Thr	TAT Tyr 285	GGC Gly	AAG Lys	TTT Phe	864
CTT Leu	GCC Ala 290	GAT Asp	GGT Gly	GGT Gly	TGC Cys	TCT Ser 295	GGG Gly	GGC Gly	GCT Ala	TAT Tyr	GAC Asp 300	ATC Ile	ATA Ile	ATA Ile	TGT Cys	912
GAT Asp 305	GAG Glu	TGC Cys	CAT His	TCA Ser	ACT Thr 310	GAC Asp	TCG Ser	ACT Thr	ACA Thr	ATC Ile 315	TTG Leu	GGC Gly	ATC Ile	GGC Gly	ACA Thr 320	. 960
										Arg		GTC Val				1008
												CCA Pro				1056
												TAT Tyr 365				1104
												ATT Ile				1152
												TCA Ser				1200
						Tyr	Arg	Gly		Asp	Val	TCC Ser				1248
												CTG Leu				1296
												ACA Thr 445				1344
												ATT Ile				1392
												CGG Arg				1440
												CCG Pro				1488

485 490 495 CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG 1536 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG 1584 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG 1632 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC 1680 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA 1728 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA 1776 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 585 TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC 1824 Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 595 GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC 1872 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 615 1920 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 GAC CTG GAG GTC GTT ACG TAG GAA TTC GAG CTC CGT CGA CAA GCT TGC 1968 Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys 645 650 GGC CGC ACT CGA GCA CCA CCA CCA CCA CTG AGA TCC 2007 Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg 660

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2007 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

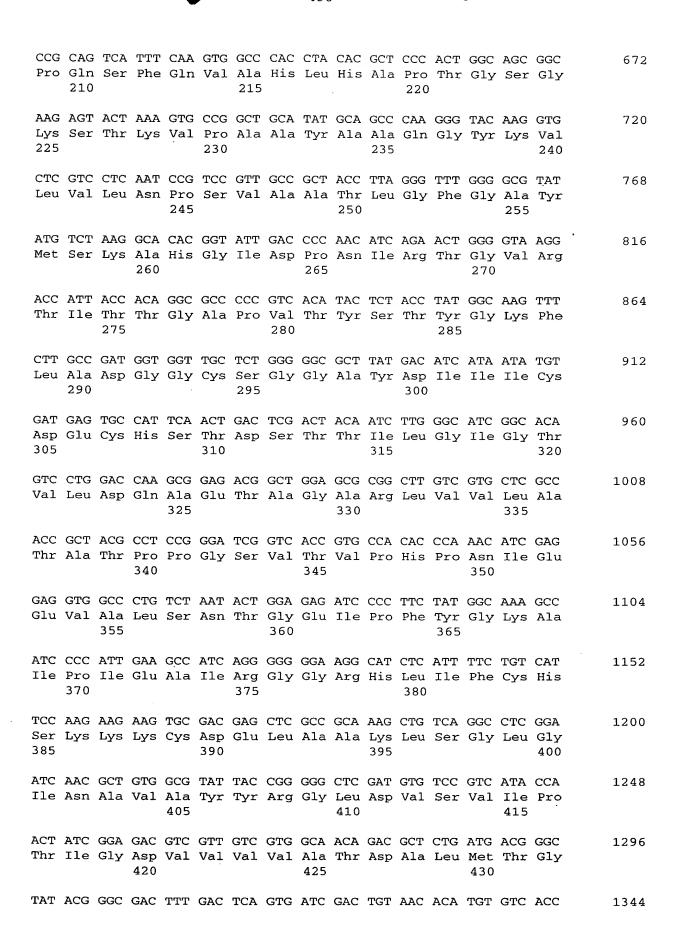
(ix) FEATURE:

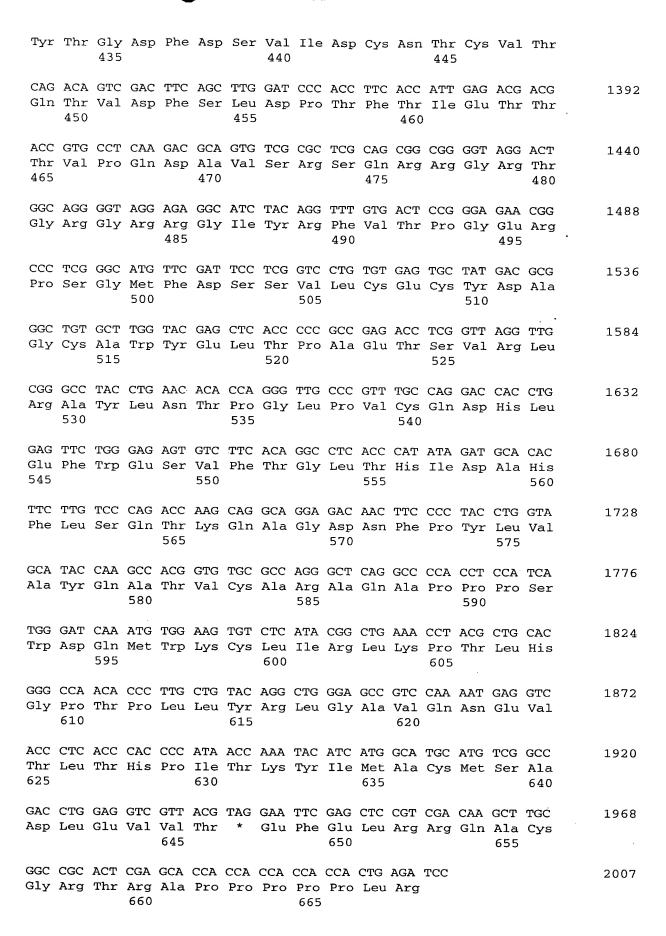
(A) NAME/KEY: CDS

(B) LOCATION: 1..2004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATG Met 1	CAT His	ATG Met	CAT His	CAT His 5	His	CAC His	CAT His	CAT His	CTG Leu 10	GTG Val	CCG Pro	CGC Arg	GGC Gly	AGC Ser 15	Ala	48
CCC Pro	ATC Ile	ACG Thr	GCC Ala 20	Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 25	Arg	GGC Gly	CTA Leu	CTT Leu	GGT Gly 30	Cys	ATC Ile	96
ATC Ile	ACT Thr	AGC Ser 35	CTT Leu	ACA Thr	GGC Gly	CGG Arg	GAC Asp 40	AAG Lys	AAC Asn	CAG Gln	GTC Val	GAG Glu 45	GGA Gly	GAG Glu	GTT Val	144
CAG Gln	GTG Val 50	GTT Val	TCC Ser	ACC Thr	GCA Ala	ACA Thr 55	CAA Gln	TCC Ser	TTC Phe	CTG Leu	GCG Ala 60	ACC Thr	TGC Cys	GTC Val	AAC Asn	192
GGC Gly 65	GTG Val	TGT Cys	TGG Trp	ACC Thr	GTT Val 70	TAC Tyr	CAT His	GGT Gly	GCT Ala	GGC Gly 75	TCA Ser	AAG Lys	ACC Thr	TTA Leu	GCC Ala 80	240
GGC Gly	CCA Pro	AAG Lys	GGG Gly	CCA Pro 85	ATC Ile	ACC Thr	CAG Gln	ATG Met	TAC Tyr 90	ACT Thr	AAT Asn	GTG Val	GAC Asp	CAG Gln 95	GAC Asp	288
CTC Leu	GTC Val	GGC Gly	TGG Trp 100	CAG Gln	GCG Ala	CCC Pro	CCC Pro	GGG Gly 105	GCG Ala	CGT Arg	TCC Ser	TTG Leu	ACA Thr 110	CCA Pro	TGC Cys	336
												CAT His 125				384
ATT Ile	CCG Pro 130	GTG Val	CGC Arg	CGG Arg	CGG Arg	GGC Gly 135	GAC Asp	AGT Ser	AGG Arg	GGG Gly	AGC Ser 140	CTG Leu	CTC Leu	TCC Ser	CCC Pro	432
												CCA Pro				480
CCT Pro	TCG Ser	GGG Gly	CAC His	GCT Ala 165	GTG Val	GGC Gly	ATC Ile	TTC Phe	CGG Arg 170	GCT Ala	GCC Ala	GTA Val	TGC Cys	ACC Thr 175	CGG Arg	528
												TCC Ser				576
ACT Thr	ATG Met	CGG Arg 195	TCT Ser	CCG Pro	GTC Val	TTC Phe	ACG Thr 200	GAC Asp	AAC Asn	TCA Ser	TCC Ser	CCC Pro 205	CCG Pro	GCC Ala	GTA Val	624





(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTIC

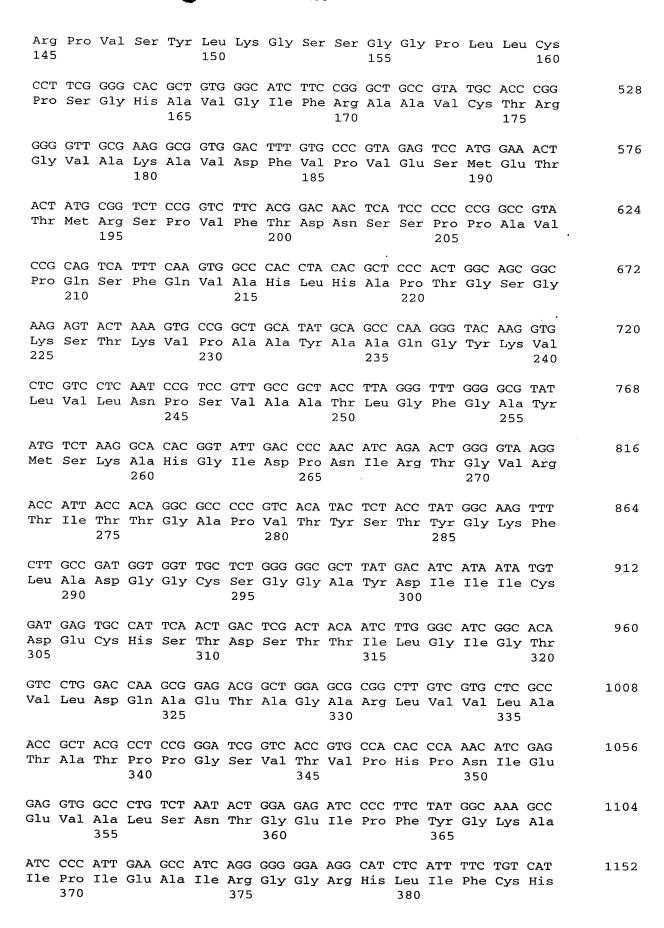
- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

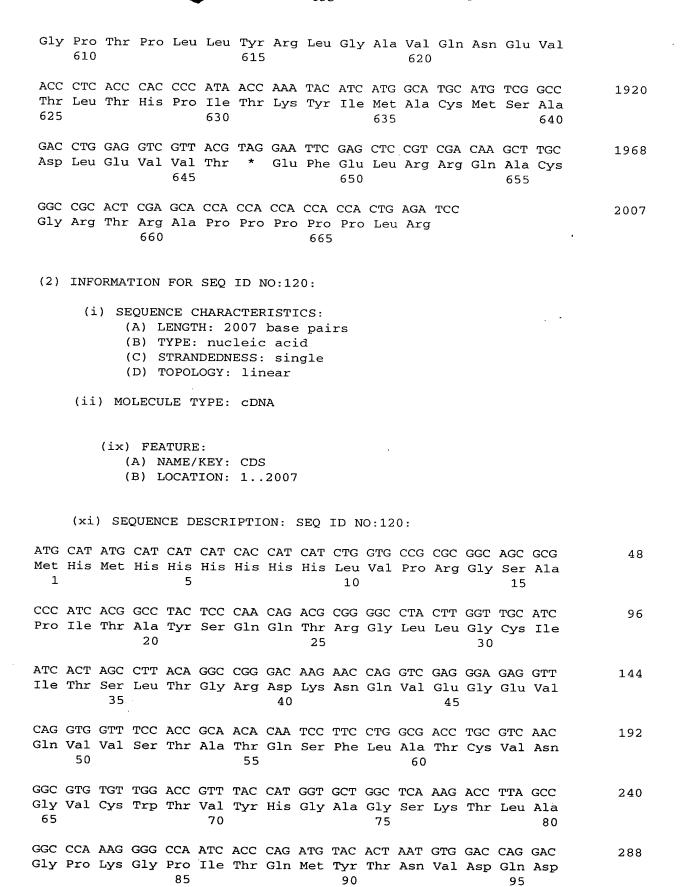
- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2004

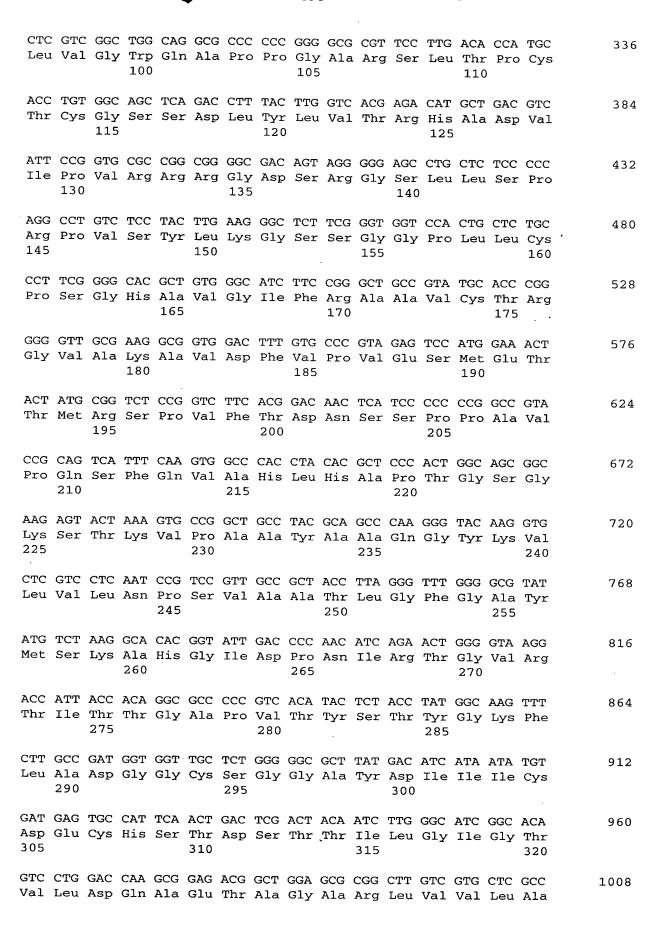
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATG Met 1	CAT His	ATG Met	CAT His	CAT His 5	CAT His	CAC His	CAT His	CAT His	CTG Leu 10	GTG Val	CCG Pro	CGC Arg	GGC Gly	AGC Ser 15	GCG Ala	4	8
CCC Pro	ATC Ile	ACG Thr	GCC Ala 20	TAC Tyr	TCC Ser	CAA Gln	CAG Gln	ACG Thr 25	CGG Arg	GGC Gly	CTA Leu	CTT Leu	GGT Gly 30	TGC Cys	ATC Ile	9	6
												GAG Glu 45				14	4
												ACC Thr				19	2
												AAG Lys				24	0
												GTG Val				28	8
												TTG Leu				33	6
												CAT His 125				38	4
												CTG Leu				43	2
AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	CTG	CTC	TGC	48	0



шаа																	
Ser 385	Lys	Lys	: AAG	: TGC	Asp 390	Glu	CTC Leu	GCC Ala	C GCA A Ala	AAG Lys 395	Leu	TCA Ser	GGC Gly	CTC Leu	GGA Gly 400	120	0
ATC Ile	AAC Asn	GCT Ala	' GTG Val	GCG Ala 405	Tyr	TAC Tyr	CGG Arg	GGG Gly	CTC Leu 410	Asp	GTG Val	TCC Ser	GTC Val	ATA Ile 415	CCA Pro	124	8 1
ACT Thr	TCC Ser	GGA Gly	GAC Asp 420	Val	GTT Val	GTC Val	GTG Val	GCA Ala 425	Thr	GAC Asp	GCT Ala	CTG Leu	ATG Met 430	Thr	GGC Gly	129	6
TAT Tyr	ACG Thr	GGC Gly 435	Asp	TTT Phe	GAC Asp	TCA Ser	GTG Val 440	Ile	GAC Asp	TGT Cys	AAC Asn	ACA Thr 445	Cys	GTC Val	ACC Thr	. 134	4
CAG Gln	ACA Thr 450	GTC Val	GAC Asp	TTC Phe	AGC Ser	TTG Leu 455	GAT Asp	CCC Pro	ACC Thr	TTC Phe	ACC Thr 460	Ile	GAG Glu	ACG Thr	ACG Thr	139	2
ACC Thr 465	GTG Val	CCT Pro	CAA Gln	GAC Asp	GCA Ala 470	GTG Val	TCG Ser	CGC Arg	TCG Ser	CAG Gln 475	CGG Arg	CGG Arg	GGT Gly	AGG Arg	ACT Thr 480	144	0
GGC Gly	AGG Arg	GGT Gly	AGG Arg	AGA Arg 485	GGC Gly	ATC Ile	TAC Tyr	AGG Arg	TTT Phe 490	GTG Val	ACT Thr	CCG Pro	GGA Gly	GAA Glu 495	CGG Arg	148	8
CCC Pro	TCG Ser	GGC Gly	ATG Met 500	TTC Phe	GAT Asp	TCC Ser	TCG Ser	GTC Val 505	CTG Leu	TGT Cys	GAG Glu	TGC Cys	тат Туг 510	GAC Asp	GCG Ala	153	6
GGC Gly	TGT Cys	GCT Ala 515	\mathtt{Trp}	TAC Tyr	GAG Glu	CTC Leu	ACC Thr 520	CCC Pro	GCC Ala	GAG Glu	ACC Thr	TCG Ser 525	GTT Val	AGG Arg	TTG Leu	158	4
CGG Arg	GCC Ala 530	TAC Tyr	CTG Leu	AAC Asn	ACA Thr	CCA Pro 535	GGG Gly	TTG Leu	CCC Pro	GTT Val	TGC Cys 540	CAG Gln	GAC Asp	CAC His	CTG Leu	163:	2
GAG Glu 545	TTC Phe	TGG Trp	GAG Glu	AGT Ser	GTC Val 550	TTC Phe	ACA Thr	GGC Gly	CTC Leu	ACC Thr 555	CAT His	ATA Ile	GAT Asp	GCA Ala	CAC His 560	1680	0
TTC Phe	TTG Leu	TCC Ser	CAG Gln	ACC Thr 565	AAG Lys	CAG Gln	GCA Ala	GGA Gly	GAC Asp 570	AAC Asn	TTC Phe	CCC Pro	TAC Tyr	CTG Leu 575	GTA Val	1728	8
GCA Ala	TAC Tyr	CAA Gľn	GCC Ala 580	ACG Thr	GTG Val	TGC Cys	GCC Ala	AGG Arg 585	GCT Ala	CAG Gln	GCC Ala	CCA Pro	CCT Pro 590	CCA Pro	TCA Ser	1776	6
TGG Trp	GAT Asp	CAA Gln 595	ATG Met	TGG Trp	AAG Lys	TGT Cys	CTC Leu 600	ATA Ile	CGG Arg	CTG Leu	AAA Lys	CCT Pro 605	ACG Thr	CTG Leu	CAC His	1824	4
GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG (CTG	GGA	GCC	GTC	CAA	ААТ	GAG	GTC	1872	2

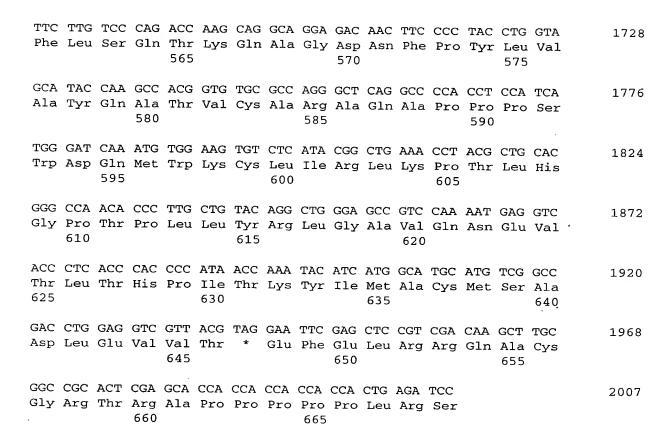




325 330 335 ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG 1056 Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu 340 345 GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC 1104 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala 355 360 ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT 1152 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His 370 375 TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA 1200 Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly 385 390 ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA 1248 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro 405 ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC 1296 Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly 420 425 TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC 1344 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG 1392 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 455 ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT 1440 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 465 470 475 480 GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG 1488 Gly Arg Gly Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg 485 CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG 1536 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG 1584 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG 1632 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC 1680 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His

555

550



(2) INFORMATION FOR SEO ID NO:121:

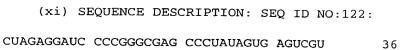
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCUCGCCCGG GGAUCCUCUA GGAAUACACG UUCGAU

36

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA (genomic)



- (2) INFORMATION FOR SEQ ID NO:123:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

 GCTCGCCCGG GGATCCTCTA G 21